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OM protein - protein search, using sw model

Run on: December 10, 2003, 20:25:06 ; Search time 11 Seconds

(without alignments)  
 115.429 Million cell updates/sec

Title: US-03-936-885-3

Perfect score: 128  
 Sequence: 1 DVKKIGTVLHKGKAALGAVADTISQ 27

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : SwissProt\_41.1\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	128	100.0	78	1	DMS1_PHYBI	P0282 phy1omedus
2	110	85.9	34	1	DMS1_PHYSA	P24302 phy1omedus
3	105	82.0	34	1	DMS2_PHYSA	P0278 phy1omedus
4	60.5	47.3	77	1	DRG2_PHYBI	Q90z5 phy1omedus
5	55.5	43.4	76	1	DMS4_PHYBI	P81486 phy1omedus
6	53.5	41.8	81	1	DMS2_PHYBI	P31107 phy1omedus
7	52.5	41.0	91	1	DRG1_PHYBI	Q90z3 phy1omedus
8	51.5	40.0	75	1	DMS2_PACDA	Q93452 pachymedusa
9	51.5	40.2	506	1	ATP0_BETVU	Q66735 beta vulgaris
10	51.5	40.2	507	1	ATP0_PEA	P05493 piatum sativum
11	51.5	40.2	508	1	ATP0_MAIZB	P05494 zea mays (m)
12	51.5	40.2	508	1	ATP0_Phaseolus	P24459 phaseolus v
13	51.5	40.2	508	1	ATP0_SOYBN	Q01915 glycine max
14	51.5	40.2	509	1	ATP0_ORGSA	P15998 oryzasativum
15	51.5	40.2	509	1	ATP0_WHETAN	P12862 triticum ae
16	51.5	40.2	510	1	ATP0_HELIANT	P18260 helianthus
17	51	39.8	334	1	RUVB_THEME	Q56313 thermotoga
18	50.5	39.5	507	1	ATP0_ARBATH	P92549 arabidopsis
19	50.5	39.5	507	1	ATP0_BRANA	P22201 brassica napus
20	50.5	39.5	507	1	ATP0_BRASA	P23413 raphanus sativus
21	50	39.1	71	1	CER1_CERCA	P36190 ceratitis c
22	50	39.1	71	1	CER2_CERCA	Q17512 ceratitis c
23	50	39.1	75	1	DMS3_AGAN	Q93223 agalychnis
24	50	39.1	144	1	MAX4_BOMX	P83083 bombyx maxima
25	50	39.1	417	1	YELM_HARIN	P44742 haemophilus
26	49.5	38.7	509	1	ATP0_NICPL	P05495 nicotiana p
27	48.5	37.9	30	1	DMS3_PHYSA	P80279 pachymedusa
28	48.5	37.9	80	1	PICDA_PICDA	Q93453 pachymedusa
29	48.5	37.9	511	1	ATP0_OENBI	P05492 oenothera biennis
30	48	37.5	495	1	MORE_XYLELLA	Q9pf85 xylorella fastidiosa
31	47	36.7	403	1	CREA_PSPFU	P38488 pseudomonas
32	47	36.7	697	1	STGB_RAUSO	Q8y213 ralstonia sphaeroides
33	46	35.9	71	1	CERD_CERCA	Q17513 ceratitis c

#### ALIGNMENTS

RESULT	1	DMS1_PHYBI	STANDARD;	PRT;	78 AA.
ID	DMS1_PHYBI				
AC	P80284;				
DT	01-FEB-1994	(Rel. 28, Created)			
DT	01-OCT-1995	(Rel. 34, Last sequence update)			
DT	15-SEP-2003	(Rel. 42, Last annotation update)			
DB	Dermaseptin BI precursor (Dermaseptin Bi)				
OS	Phylomedusa bicolor (Two-colored leaf frog)				
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae; Phylomedusidae; Phylomedusa; Phylomedusidae				
OX	NCBI_TaxID=8393;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Skin;				
RX	Medline=9429491; PubMed=8074751;				
RA	Amidie M., Ducanceau F., Mor A., Boulaïn J.C., Menez A., Nicolas P.;				
RT	"precursors of vertebrate peptide antibiotics dermaseptin b and adenoregulin have extensive sequence identities with precursors of opioid peptides dermorphin, dermenkephalin, and deltorphins."				
RL	J. Biol. Chem. 269:17847-17852(1994).				
RN	[2]				
RP	SEQUENCE OF 45-75.				
RC	TISSUE=Skin secretion;				
RX	Medline=94139616; PubMed=8306981;				
RA	Mor A., Nicolas P.;				
RT	"Isolation and structure of novel defensive peptides from frog skin."				
RL	Eur. J. Biochem. 219:145-149 (1994).				
CC	"1- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST BACTERIA, FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE FUNCTIONS WITH ITS AMPHIPATIC STRUCTURE.				
CC	"1- SUBCELLULAR LOCATION: Secreted.				
CC	"1- TISSUE SPECIFICITY: Skin.				
CC	"1- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.				
CC	Dermaseptin subfamily.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.ebi-sib.ch/announce/ or send an email to license@ebi-sib.ch).				
CC	BMBL: X72387, CAA51080.1; ...				
DR	PIR: A53727, A53727.				
DR	PIR: B54897, B54897.				
DR	InterPro: IPR04275, Brevenin.				
DR	Pfam: PF03022, Brevenin_1.				
KW	Amphibian defense peptide; Antibiotic; Fungicide; Multigene family;				
KW	Signal; Cleavage on pair of basic residues; Amidation.				
FT	POTENTIAL	1			
FT	PROPEP	23			
FT	CHAIN	45			
FT	PROPEP	76			
	DERMASEPTIN BI.	78			

FT MOD\_RES 75 75 AMIDATION (G-76 PROVIDE AMIDE GROUP)  
 PT PRT; 8700 MW; BB3B6P03058FBC6F CRC64;  
 SQ SEQUENCE 78 AA; Best Local Similarity 100.0%; Score 128; DB 1; Length 78;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DVLKIGTVHALGKALGAVADTISQ 27  
 Db 49 DVLKIGTVHALGKALGAVADTISQ 75

RESULT 2  
 DMS1\_PHYSA ID DMS1\_PHYSA STANDARD; PRT; 34 AA.  
 AC P24302; PR0277;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 \* RL Dermaseptin 1 (DS I)  
 OS Phylomedusa sauvagei (Sauvage's leaf frog)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Phylomedusinae; Phylomedusa.  
 OX NCBI\_TaxID=8395;  
 RN [1]  
 RP  
 SEQUENCE.  
 RC TISSUE=Skin secretion; MEDLINE=91363376; PubMed=1905573;  
 RX Mor A., Nguyen V.H., Defour A., Migliore-Samour D., Nicolas P.;  
 RA "Isolation, amino acid sequence, and synthesis of dermaseptin, a  
 RT novel antimicrobial peptide of amphibian skin.",  
 \* RL Biochemistry 30:8824-8830(1991).  
 RN [2]  
 RP  
 SEQUENCE.  
 RC TISSUE=Skin secretion; MEDLINE=9413986; PubMed=8306981;  
 RX Mor A., Nicolas P.;  
 RA "Isolation and structure of novel defensive peptides from frog skin.",  
 Eur J. Biochem. 219:145-154(1994).  
 CC FUNCTION: POSSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST  
 CC BACTERIA Fungi AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE  
 CC FUNCTIONS WITH ITS AMPHIPATRIC STRUCTURE.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- TISSUE SPECIFICITY: Skin.  
 CC -|- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.  
 CC Dermaseptin subfamily.

Query Match 85.9%; Score 110; DB 1; Length 34;  
 Best Local Similarity 84.6%; Pred. No. 6.2e-09;  
 Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VLKKIGTVHALGKALGAVADTISQ 27  
 Db 6 MLKDGTMHALGKALGAAADTISQ 31

RESULT 4  
 DRG2\_PHYBI ID DRG2\_PHYBI STANDARD; PRT; 77 AA.  
 AC Q902K5;  
 DT 15-SEP-2003 (Rel. 42, Created)  
 DT 15-SEP-2003 (Rel. 42, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 \* RL DRG2 precursor (Dermaseptin 2).  
 GN DRG2.  
 OS Phylomedusa bicolor (Two-colored leaf frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Phylomedusinae; Phylomedusa.  
 OX NCBI\_TaxID=8393;  
 RN [1]  
 RP  
 SEQUENCE FROM N.A.  
 RC TISSUE=Skin; AMICHE M.;  
 RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -|- FUNCTION: Has antimicrobial activity (Potential).  
 CC -|- SUBCELLULAR LOCATION: Secreted (Probable).  
 CC -|- TISSUE SPECIFICITY: Skin.  
 CC -|- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.  
 CC Dermaseptin subfamily.

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CC

48 Local Similarity 53.8%; Pred. No. 0.092; 5; Mismatches 6; Indels 1; Gaps 1;  
 Matches 14; Conservative 5; Last sequence update) Qy 3 LKKIGTVL-HAGKAALGAVADTISQ 27  
 Db 51 IIEKGAALTAAGKAALGAVADTISQ 27

DT 01-OCT-1994 (Rel. 3.0, Last sequence update)  
 DT 15-SEP-2003 (Rel. 4.2, Last annotation update)  
 DE Adenoregulin precursor (Dermaseptin BIV) (Dermaseptin B2).  
 OS Phylomedusa bicolor ("Two-colored leaf frog").  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Phylomedusinae; Phylomedusa.  
 NCBI\_TaxID:8393;  
 RN [1] NCBITaxID:8393;

RESULT 5  
 DMS4\_PHYBI STANDARD: ERT; 76 AA.

AC P81486;  
 DT 16-OCT-2001 (Rel. 4.0, Created)  
 DT 16-OCT-2003 (Rel. 4.0, Last sequence update)  
 DT 15-SEP-2003 (Rel. 4.2, Last annotation update)  
 DE Dermaseptin BIV precursor (Dermaseptin-B4).  
 OS Phylomedusa bicolor ("Two-colored leaf frog").  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Phylomedusinae; Phylomedusa.  
 RN NCBITaxID:8393;

RN SEQUENCE FROM N.A., SEQUENCE OF 46-73, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=98278974; PubMed=9614066;  
 RA Charpentier S.; Amice M.; Messer J.; Vouille V.; Le Caer J.-P.,  
 RA Nicolas P.; DelFour A.;  
 RT "Structure, synthesis, and molecular cloning of dermaseptins B, a  
 family of skin peptide antibiotics";  
 RL J. Biol. Chem. 273:14690-14697 (1998).  
 CC -I- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST GRAM-  
 CC POSITIVE AND GRAM-NEGATIVE BACTERIA. PROBABLY ACTS BY DISTURBING  
 CC MEMBRANE FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- TISSUE SPECIFICITY: Skin.  
 CC -I- MASS SPECTROMETRY: MW=2997.15; MW\_BRR=0.1; METHOD=Electrospray.  
 CC -I- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.  
 CC -I- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.  
 CC -I- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.

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CC -I- TISSUE SPECIFICITY: Skin.  
 CC -I- FUNCTION: ENHANCES BINDING OF AGONISTS TO ADENOSINE RECEPTORS.  
 CC -I- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.  
 CC -I- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.  
 CC -I- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.

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CC -I- TISSUE SPECIFICITY: Skin.  
 CC -I- FUNCTION: ENHANCES BINDING OF AGONISTS TO ADENOSINE RECEPTORS.  
 CC -I- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.  
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CC -I- TISSUE SPECIFICITY: Skin.  
 CC -I- FUNCTION: ENHANCES BINDING OF AGONISTS TO ADENOSINE RECEPTORS.  
 CC -I- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.

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DT 01-OCT-1994 (Rel. 3.0, Last sequence update)

DT 15-SEP-2003 (Rel. 4.2, Last annotation update)

DE Adenoregulin precursor (Dermaseptin BIV) (Dermaseptin B2).

OS Phylomedusa bicolor ("Two-colored leaf frog").

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;

OC Phylomedusinae; Phylomedusa.

NCBI\_TaxID:8393;

RN [1] SEQUENCE FROM N.A.

RC TISSUE=Skin secretion;

RX MEDLINE=93066363; PubMed=1438101;

RA Amiche M.; Ducarrel F.; Lajeunesse E.; Boulain J.-C.; Menez A.,

RA Nicolas P.; Molecular cloning of a cDNA encoding the precursor of adenoregulin

from frog skin. Relationships with the vertebrate defensive peptides,

"dermaseptins".

RT Biochem. Biophys. Res. Commun. 191:983-990 (1993).

[2]

RN SEQUENCE OF 46-78.

RC TISSUE=Skin secretion;

RX MEDLINE=93066363; PubMed=1438101;

RA Daly J.W.; Caceres J.; Moni R.W.; Gusovsky F.; Moos M. Jr.,

RA Seamon K.B.; Milton K.; Myers C.W.,

RA "Frog secretions and hunting magic in the upper Amazon:

identification of a peptide that interacts with an adenosine receptor".

RT Proc. Natl. Acad. Sci. U.S.A. 89:10960-10963 (1992).

[3]

RN SYNTHESIS, AND CHARACTERIZATION.

RC TISSUE=Skin;

RX MEDLINE=94139686; PubMed=8306981;

RA Mor A.; Nicolas P.,

RT "Isolation and structure of novel defensive peptides from frog skin."

Biochim. Biophys. Acta 219:145-154 (1994).

CC -I- FUNCTION: ENHANCES BINDING OF AGONISTS TO ADENOSINE RECEPTORS.

CC -I- POSITION: POSSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST

BACTERIA, FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE

FUNCTONS WITH ITS AMPHIPATHIC STRUCTURE.

CC -I- SUBCELLULAR LOCATION: Secreted.

CC -I- TISSUE SPECIFICITY: Skin.

CC -I- DISEASE: AFFECTS HUMAN BEHAVIOR ELICITING PROFOUND MALAISE,

CC FOLLOWED BY LISTLESSNESS AND THEN EUPHORIA.

CC -I- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.

CC -I- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.

CC -I- SUBCELLULAR LOCATION: Secreted.

CC -I- TISSUE SPECIFICITY: Skin.

CC -I- FUNCTION: ENHANCES BINDING OF AGONISTS TO ADENOSINE RECEPTORS.

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CC -I- SUBCELLULAR LOCATION: Secreted.

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CC -I- SUBCELLULAR LOCATION: Secreted.

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BACTERIA, FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE

FUNCTONS WITH ITS AMPHIPATHIC STRUCTURE.

CC -I- SUBCELLULAR LOCATION: Secreted.

CC -I- TISSUE SPECIFICITY: Skin.

CC -I- FUNCTION: ENHANCES BINDING OF AGONISTS TO ADENOSINE RECEPTORS.

CC -I- POSITION: POSSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST

BACTERIA, FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE

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EMBL; D15055; BRA03664.1; -
PIR; S33922; S33922.
HSSP; P19483; 1BMF.
InterPro; IPR00793; ATPase_a/bC.
InterPro; IPR00194; ATPase_a/bcentre.
InterPro; IPR00190; ATPase_a/bN.
InterPro; IPR00790; ATPase_ac.
InterPro; IPR05294; ATPsynthF1_alpha.
PFam; PF00006; ATP_bynt_ab; 1.
PFam; PF00306; ATP_bynt_ab_C; 1.
PFam; PF02874; ATP_bynt_ab_N; 1.
ProDom; P0001039; ATPase_aC; 1.
TIGR3DB; TIGR0962; atpa; 1.
PROSITE; PS00122; ATPase_ALPHA_BETA; 1.
ATP synthesis; CF(1); Hydrogen-ion transport;
Hydratase; ATP-binding; Mitochondrion.
NP_BIND_178 ATP BY SIMILARITY.
ACT_SITE_373 373 ATP BY SIMILARITY.

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BUILT-10	20_PEA	ATPO	PEA	P05453;	STANDARD;	PRT;	507 AA.
				01-NOV-1988	(Rel. 09, Created)		
				01-JUN-1994	(Rel. 29, Last sequence update)		
				28-FEB-2003	(Rel. 41, Last annotation update)		
				ATP synthase alpha chain, mitochondrial	(EC 3.6.3.14)		

*Pisum sativum* (Garden pea).  
Mitochondrion.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
euRosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.  
NCBI\_TaxID=38888; [1]

STRAINACV, Alabama; MEDLINE=8727992; PubMed=2886497; Morikami A, Nakamura K; "Structure and expression of pea mitochondrial F1ATPase alpha-subunit gene and its pseudogene involved in homologous recombination." J. Biochem. 101: 967-976 (1987)

<sup>1</sup>-SEQUENCE FROM N.A.  
STRAIN=CV, Alaska;  
MEDLINE=94033880; PubMed=7764223;  
Morikami A., Nakamura K.;  
"Transcript map of oppositely oriented pea mitochondrial genes  
encoding the alpha-subunit and the subunit 9 of F1FO-ATPase  
complex.",  
Biotechnol. Biochem. 57:1530-1535(1993).  
-1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON  
GRADIENT ACROSS THE MEMBRANE. THE ALPHA CHAIN IS A REGULATORY

-1 - CATALYTIC ACTIVITY: ATP + H<sub>2</sub>O + H<sup>(+)</sup> (In) = ADP + phosphate + H<sup>(+)</sup> (Out).

-1 - SUBUNIT: P-TYPE ATPASES HAVE 2 COMPONENTS, CP(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CP(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CP(0) HAS THREE MAIN SUBUNITS: A, B AND C.

-1 - SUBCELLULAR LOCATION: Mitochondrial

-1 - SIMILARITY: Belongs to the ATPase alpha/beta chains family.

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EMBL; X03366; CAA28864.1; -.
EMBL; D1698; BAA03324.1; -.
PIR; A26760; A26760.
PIR; JN0769; JN0769.
HSSP; P19483; 1BMF.
InterPro; IPR000793; ATPase_abC.
InterPro; IPR000194; ATPase_abcentre.
InterPro; IPR004100; ATPase_abN.
InterPro; IPR000790; ATPase_ac.
InterPro; IPR000791; ATPase_ac.
InterPro; IPR000792; ATPase_ac.

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Pfam: PF0006; ATP-synt_ab; 1.
Pfam: PF00306; ATP-synt_ab_C; 1.
Pfam: PF02874; ATP-synt_ab_N; 1.
Pfam: PD001059; ATPase_AC; 1.
TIGRFAMs: TIGR00962; ATPase; 1.
PROSITE: PS00152; ATPase_Alpha_Beta; 1.

ATP synthase; ATP-binding; Mitochondrion.
Hydrolyase; ATPase; ATP (BY SIMILARITY).
NP BIND ACT SITE 171 178 ATP (BY SIMILARITY).
SEQUENCE 50045 MW: 2244806728661D1 C8C64.
          373 373 BY SIMILARITY.

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    try Match      40.2%;  Score 51.5;  DB 1;  Length 507;
    t Local Similarity 42.3%;  Fred. No. 8.4;
    matches 11;  Conservative 7;  Mismatches 7;  Indels 1;  Gaps
    1 DVLKIGITVA-LHAGKAALGNAVADTI 25
    88 DATUMSGCSTYNDUOAKOMI QPBDVDTI 113

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T 11  
P05-94; ATPO MAIZE STANDARD; PRT; 508 AA.  
01-NOV-1988 (Rel. 09, Created)  
01-Nov-1988 (Rel. 00, Incl.)  
01-Nov-1988 (Rel. 00, Incl.)

*Zea mays* (Maize).  
Mitochondrion.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
ATPA. ATP synthase alpha chain, mitochondrial (EC 3.6.3.14).  
ATPA. Last annotation update)

NCBI\_TaxID=4577;  
[1] SEQUENCE FROM N.A.  
Braun C.J., Levings C.S. III;  
"Nucleotide sequence of the F1-ATPase alpha subunit from maize  
mitochondria";  
Plant Physiol., 79:571-577(1985).  
[2] SEQUENCE FROM N.A.  
MEDLINE:A8311189; PubMed:2900697.

"The mitochondrial genome of fertile maize (*Zea mays* L.) contains two copies of the gene encoding the alpha-subunit of the F1-ATPase.";

RT Curr. Genet. 10:321-328 (1985).

RT -I- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE ALPHA CHAIN IS A REGULATORY SUBUNIT.

CC -I- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate + H(+) (Out).

CC -I- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CP(0) - THE MEMBRANE PROTON CHANNEL, CP(1) HAS FIVE SUBUNITS: ALPHA (3), BETA (3), GAMMA (1), DELTA (1), EPSILON (1). CP(0) HAS THREE MAIN SUBUNITS: A, B AND C.

CC -I- SUBCELLULAR LOCATION: Mitochondrial.

CC -I- SIMILARITY: Belongs to the ATPase alpha/beta chains family.

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DR EMBL; M16222; AA07269\_1; -.

DR BMBL; 2000036; CRA77319\_1; -.

DR PIR; A23757; PW2NAM.

DR HSSP; P19483; IEMF.

DR Maizeds; 69198; -.

DR InterPro; IPR000793; ATPase\_a/bC.

DR InterPro; IPR000194; ATPase\_a/bcentre.

DR InterPro; IPR000100; ATPase\_a/bN.

DR InterPro; IPR000790; ATPase\_aC.

DR InterPro; IPR000790; ATPase\_aC.

DR Pfam; PF00006; ATP-Synt\_ab\_C.

DR Pfam; PF000106; ATP-Synt\_ab\_C.

DR Prodrom; PP02874; ATP-Synt\_ab\_N.

DR Prodrom; PD001093; ATPase\_aC.

DR TIGRFAMs; TIGR00962; ATPA.

DR PROSITE; PS00152; ATPase\_ALPHA\_BETA; 1.

KW ATP synthase; CP(1); ALPHA\_BETA; 1.

KW ATP synthase; CP(1); Hydrogen Ion transport;

KW Hydrolase; ATP-binding; Mitochondrion.

PT NP\_BIND

PT ACT\_SITE

SEQUENCE 508 AA; 55180 MW; PBADD33141A0456 CRC64;

Query Match Score 51.5; DB 1; Length 508;

Best Local Similarity 42.3%; Pred. No. 8.4;

Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1; Gaps 1;

Qy 1 DVLKKGTVLAHAGKAALGAVADTI 25

Db 88 DLVKKGTVLAHAGKAALGAVADTI 25

88 DLVKKGTVLAHAGKAALGAVADTI 25

SEQUENCE 508 AA; 2198F396BEBCCA79 CRC64;

Query Match Score 51.5%; DB 1; Length 508;

Best Local Similarity 42.3%; Pred. No. 8.4;

Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1; Gaps 1;

Qy 1 DVLKKGTVLAHAGKAALGAVADTI 25

Db 88 DLVKKGTVLAHAGKAALGAVADTI 25

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Db 88 DLVKKGTVLAHAGKAALGAVADTI 25

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Query Match Score 51.5%; DB 1; Length 508;

Best Local Similarity 42.3%; Pred. No. 8.4;

Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1; Gaps 1;

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Query Match Score 51.5%; DB 1; Length 508;

Best Local Similarity 42.3%; Pred. No. 8.4;

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Db 88 DLVKKGTVLAHAGKAALGAVADTI 25

SEQUENCE 508 AA; 2198F396BEBCCA79 CRC64;

Query Match Score 51.5%; DB 1; Length 508;

Best Local Similarity 42.3%; Pred. No. 8.4;

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Db 88 DLVKKGTVLAHAGKAALGAVADTI 25

SEQUENCE 508 AA; 2198F396BEBCCA79 CRC64;

Query Match Score 51.5%; DB 1; Length 508;

Best Local Similarity 42.3%; Pred. No. 8.4;

Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1; Gaps 1;

Qy 1 DVLKKGTVLAHAGKAALGAVADTI

recombination repeats and multiple transcripts at the *atpa* loci.";

AL Curr. Genet. 23:234-247(1993).

CC -1- FUNCTION: PRODUCES ATP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE ALPHA CHAIN IS A REGULATORY SUBUNIT.

CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate + H(+) (Out).

CC -1- SUBUNITS: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA (3), BETA (3), GAMMA (1), DELTA (1), EPSILON (1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.

CC -1- SUBCELLULAR LOCATION: Mitochondrial.

CC -1- SIMILARITY: Belongs to the ATPase alpha/beta chains family.

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DR EMBL; 214031; CAA78407.1; - .

DR ETR; S29792; S29792.

DR HSSP; P19483; 1BMP.

DR InterPro; IPR000793; ATPase\_a/bC.

DR InterPro; IPR000194; ATPase\_a/bcentre.

DR InterPro; IPR000100; ATPase\_a/bN.

DR InterPro; IPR000790; ATPase\_aC.

DR InterPro; IPR005294; ATPsynthF1\_alpha.

DR Pfam; PF00016; ATP-BNt\_ab; 1.

DR Pfam; PF00016; ATP-BNT\_ab\_C; 1.

DR Pfam; PF0274; ATP-BNT\_ab\_N; 1.

DR Prodrom; PD001093; ATPase\_aC; 1.

DR TIGRFAM; TIGR00962; atpa; 1.

DR PROSITE; PS00152; ATPase\_ALPHA\_BETA; 1.

KW ATP synthetis; CF(1); Hydrogen Ion transport;

KW Hydrolase; ATP-binding; Mitochondrion.

FT NP BIND 171 178 ATP (BY SIMILARITY).

FT ACT SITE 373 373 BY SIMILARITY.

SEQUENCE 508 AA; 55330 MW; C70C73CC3c6D314F: CR64;

Query Match Score 51.5; DB 1; Length 509;

Best Local Similarity 42.3%; Pred. No. 8.4;

Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

Qy 1 DVKKIGTVLAHAGAALGAVADTI 25

Db 88 DLVKRTGSIVDVPAKGMLGRVVDAL 113

RESULT 14

ATPO\_ORYSA STANDARD; PRT; 509 AA.

AC P15558 /

DT 01-APR-1980 (Rel. 14, Created)

DT 01-APR-1980 (Rel. 14, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DB ATP synthase alpha chain, mitochondrial (EC 3.6.3.14).

GN ATPA.

O8 Oriza sativa (Rice).

OG Mitochondria.

OC Bukaryota; Viridiplantae; Streptophyta; Embryophyt; Tracheophyt;

OC Spermatophyt; Magnoliophyt; Liliopsida; Poales; Poaceae;

OX NCBI\_TAXID=4530;

RN [1] \_

RP SEQUENCES FROM N.A.

RC STRAIN=CV; Japonica; TISSUE=Shoot;

RX MEDLINE=902668; PubMed=213830;

RA Kadokawa K.I.; Boireau P.; Laporte J.;

RT "Nucleotide sequence of the PI-ATPase alpha subunit gene from rice mitochondria.",

RL Nucleic Acids Res. 18:1302-1302(1990).

CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE ALPHA CHAIN IS A REGULATORY SUBUNIT.

CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate + H(+) (Out).

CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA (3), BETA (3), GAMMA (1), DELTA (1), EPSILON (1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.

CC -1- SUBCELLULAR LOCATION: Mitochondrial.

CC -1- SIMILARITY: Belongs to the ATPase alpha/beta chains family.

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DR EMBL; X51422; CAA35787.1; - .

DR PIR; JO0411; PWZBM.

DR HSSP; P19483; 1BMP.

DR ANU-2DPAGE; P1598;

DR Gramene; P1599;

DR InterPro; IPR000193; ATPase\_a/bC.

DR InterPro; IPR000194; ATPase\_a/bcentre.

DR InterPro; IPR000194; ATPase\_a/bN.

DR InterPro; IPR00100; ATPase\_a/bN.

DR InterPro; IPR00090; ATPase\_AC.

DR InterPro; IPR005294; ATPsynthF1\_alpha.

DR Pfam; PF00006; ATP-Synth\_ab; 1.

DR Pfam; PF00006; ATP-Synth\_ab; 1.

DR Pfam; PF00016; ATP-Synth\_ab\_C; 1.

DR Prodrom; PD001093; ATP-Synth\_ab\_N; 1.

DR TIGRFAM; TIGR00962; atpa; 1.

DR PROSITE; PS00152; ATPase\_ALPHA\_BETA; 1.

KW ATP Synthetis; CF(1); Hydrogen Ion transport;

KW Hydrolase; ATP-bind; Mitochondrion.

FT NP BIND 171 178 ATP (BY SIMILARITY).

FT ACT SITE 373 373 BY SIMILARITY.

FT SEQUENCE 509 AA; 7E6C7561B7C0668 CRC64;

Query Match Score 51.5; DB 1; Length 509;

Best Local Similarity 42.3%; Pred. No. 8.4;

Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

Qy 1 DVKKIGTVLAHAGAALGAVADTI 25

Db 88 DLVKRTGSIVDVPAKGMLGRVVDAL 113

RESULT 15

ATPO\_WHEAT STANDARD; PRT; 509 AA.

ID ATPO\_WHEAT STANDARD;

ID ATPO\_WHEAT STANDARD;

AC P12852 /

DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DB ATP synthase alpha chain, mitochondrial (EC 3.6.3.14).

GN ATPA.

OS Triticum aestivum (Wheat).

OS Mitochondrion.

OC Bukaryota; Viridiplantae; Streptophyta; Embryophyt; Tracheophyt;

OC Spermatophyt; Magnoliophyt; Liliopsida; Poales; Poaceae;

OX NCBI\_TAXID=4565;

RN [1] \_

RP SEQUENCE FROM N.A.

RX MEDLINE=90016324; PubMed=2529479;

RA Schulte B.; Staubach S.; Laser B.; Kueck U.;

RT "What mitochondrial DNA: organization and sequences of the atpA and atp9 genes.";

Search completed: December 10, 2003, 20:28:06  
Job time : 12 sec

Copyright GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 10, 2003, 20:26:11 ; Search time 21. Seconds  
(without alignments)  
123.845 Million cell updates/sec

Title: US-09-936-885-3

Perfect score: 128

Sequence: 1 DVLKKIGTVLHALGKAALGAVADTISQ 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters:

283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : PIR\_76;\*

1: Pir1;\*

2: Pir2;\*

3: Pir3;\*

4: Pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	128	100.0	27	2	AS3727		dermaseptin b - tw
2	128	100.0	78	2	B54897		dermaseptin b I or
3	110	85.9	34	2	A40298		dermaseptin - Savu
4	53.5	41.8	81	1	JN0462		adenoregulin precursor
5	51.5	40.2	327	4	S29876		probable H+ transporter
6	51.5	40.2	506	2	S33922		H+ -transporting tw
7	51.5	40.2	506	2	S46508		H+ -transporting tw
8	51.5	40.2	507	2	JN0769		H+ -transporting tw
9	51.5	40.2	507	2	A26760		H+ -transporting tw
10	51.5	40.2	508	1	PWZMAM		H+ -transporting tw
11	51.5	40.2	508	2	S26979		H+ -transporting tw
12	51.5	40.2	508	1	S29792		H+ -transporting tw
13	51.5	40.2	509	1	PWMTAM		H+ -transporting tw
14	51.5	40.2	509	1	PWZAM		H+ -transporting tw
15	51.5	40.2	510	2	S10997		H+ -transporting tw
16	51.5	40.2	510	2	S19261		H+ -transporting tw
17	51	39.8	334	2	A72217		Holliday junction
18	50.5	39.5	507	1	PWRPA		H+ -transporting tw
19	50.5	39.5	507	2	S12309		arginyl-tRNA synth
20	50.5	39.5	590	2	A96691		hypothetical prote
21	50	39.1	417	2	A64154		H+ -transporting tw
22	49.5	38.7	509	1	PWNATC		purine nucleoside
23	49	38.3	236	2	G9007		probable transcript
24	49	38.3	256	2	F83103		hypothetical prote
25	48.5	37.9	317	2	H70805		H+ -transporting tw
26	48.5	37.9	491	2	S17916		hypothetical prote
27	48.5	37.9	511	2	S07316		H+ -transporting tw
28	48	37.5	396	2	H97500		conserved hypothet
29	48	37.5	396	2	AD2719		gene atpA, intron 2

## ALIGNMENTS

RESULT 1		RESULT 2	
AS3727	dermaseptin b - two-colored leaf frog	Qy	1 DVLLKIGTVLHALGKAALGAVADTISQ 27
C;Species: Phylomedusa bicolor (two-colored leaf frog)	C;Species: Phylomedusa bicolor (two-colored leaf frog)	Db	1 DVLLKIGTVLHALGKAALGAVADTISQ 27
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Apr-1998	C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999		
R;Mor, A.; Amiche, M.; Nicolas, P.	R;Amiche, M.; Ducane, F.; Mor, A.; Boulain, J.C.; Menez, A.; Nicolas, P.		
A;Title: Structure, synthesis, and activity of dermaseptin b, a novel vertebrate defensin	J. Biol. Chem. 269, 17847-17852, 1994		
A;Reference number: A53727	A;Accession: A53727		
A;Status: Preliminary	A;Title: Precursors of vertebrate peptide antibiotics dermaseptin b and adrenoregulin have a modified site: amidated carboxyl end (Gln). (amide in mature form from following g1)		
A;Molecule type: protein	A;Accession: B54897		
A;Residues: 1-27	A;Molecule type: mRNA		
A;Cross-references: GB:X72387; NID:9505483; PID:CA51080.1; PMID:94299491; PM	A;Cross-references: GB:X72387; NID:9505483; PID:CA51080.1; PMID:94299491; PM		
C;Superfamily: dermaseptin precursor; dermorphin precursor amino-terminal homology	C;Superfamily: dermaseptin precursor; dermorphin precursor amino-terminal homology		
C;Keywords: amidated carboxyl end; antibiotic; antimicrobial; skin	C;Keywords: amidated carboxyl end; antibiotic; antimicrobial; skin		
F1-14/Domain: dermaseptin precursor amino-terminal homology <DER>	F1-14/Domain: dermaseptin precursor amino-terminal homology <SIG>		
F23-44/Domain: signal sequence #status predicted <PRO>	F23-44/Domain: signal sequence #status predicted <PRO>		
F149-75/Product: dermaseptin b I #status experimental <MAT>	F149-75/Product: dermaseptin b I #status experimental <MAT>		
F775/Modified site: amidated carboxyl end (Gln). (amide in mature form from following g1)	F775/Modified site: amidated carboxyl end (Gln). (amide in mature form from following g1)		
Query Match Score 100.0%; DB 2; Length 27;	Query Match Score 100.0%; DB 2; Length 27;		
Best Local Similarity 100.0%; Pred. No. 6.9e-12; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity 100.0%; Pred. No. 6.9e-12; Mismatches 0; Indels 0; Gaps 0;		

RESULT 3

Qy 1 DVLKKGTVVALHGGKAALGAVADTISQ 27  
C;Species: Phylomedusa sauvagei (Sauvage's leaf frog)  
C;Date: 13-May-1992 #sequence\_revision 13-May-1992 #text\_change 09-Apr-1996  
C;Accession: A40298  
R;Mor, A.; Nguyen, V.H.; Delfour, A.; Migliore-Samour, D.; Nicolas, P.  
Biochemistry 30, 8824-8830, 1991  
A;Title: Isolation, amino acid sequence, and synthesis of dermaseptin, a novel antimicrobial peptide.  
A;Reference number: A40298; MUID:91363376; PMID:1909573  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-34 <MOR>  
C;Superfamily: dermaseptin precursor; dermorphin precursor amino-terminal homology  
C;Keywords: skin

Query Match Score 85.9%; Best Local Similarity 84.6%; Pred. No. 3.4e-09;  
Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VLKKIGTVVALHGGKAALGAVADTISQ 27  
Db 6 MLKKLGTMVALHGGKAALGAVADTISQ 31

RESULT 4

JN0462 adrenoregulin precursor - two-colored leaf frog

C;Species: Phylomedusa bicolor (two-colored leaf frog)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: JN0462; A54697; K4171; S4718  
R;Amiche, M.; Ducaneil, F.; Lajeunesse, E.; Boulain, J.C.; Menez, A.; Nicolas, P.  
Biochem. Biophys. Res. Commun. 191, 983-990, 1993  
A;Title: Molecular cloning of a cDNA encoding the precursor of adrenoregulin from frog skin  
A;Reference number: JN0462; MUID:93221546; PMID:8466537  
A;Accession: A54692  
A;Molecule type: mRNA  
A;Residues: 1-81 <AM2>  
A;Cross-references: EMBL:X70278; PIDN:CAA49763\_1; PID:9395932  
A;Experimental source: skin  
A;Note: the authors translated the codon AAA for residue 26 as Leu  
R;Amiche, M.; Ducaneil, F.; Mor, A.; Boulain, J.C.; Menez, A.; Nicolas, P.  
J. Biol. Chem. 269, 17847-17852, 1994  
A;Title: Precursors of vertebrate peptide antibiotics dermaseptin b and adrenoregulin have identical primary structures  
A;Reference number: A54697; MUID:9429991; PMID:8074751  
A;Accession: A54697  
A;Molecule type: mRNA  
A;Residues: 1-81 <AM2>  
A;Cross-references: GB:X70278; PIDN:CAA49763\_1; PID:g395932  
R;Daly, J.W.; Caceres, J.; Moni, R.W.; Gusovsky, F.; Moos Jr., M.; Seamon, K.B.; Milton, Proc. Natl. Acad. Sci. U.S.A. 89, 10966-10963, 1992  
A;Title: Frog secretions and hunting magic in the upper Amazon: identification of a peptide  
A;Reference number: A44171; MUID:93066363; PMID:1438301  
A;Accession: A44171  
A;Molecule type: protein  
C;Superfamily: dermaseptin precursor; dermorphin precursor amino-terminal homology  
C;Keywords: antibiotic, antifungal, skin  
P;1-45/Domain: dermorphin precursor amino-terminal homology <DER>  
P;1-22/Domain: signal sequence #status predicted <SIG>  
P;23-45/Domain: propeptide #status predicted <PRO>  
P;46-78/Product: adrenoregulin #status experimental <MAT>

Query Match Score 41.8%; Best Local Similarity 40.0%; Pred. No. 1.1%;  
Matches 12; Conservative 7; Mismatches 6; Indels 5; Gaps 1;

RESULT 5

S29876 probable H+-transporting ATP synthase pseudogene - soybean  
C;Species: Glycine max (soybean)  
C;Date: 12-Mar-1999 #sequence\_revision 12-Mar-1999 #text\_change 19-May-2000  
C;Accession: S29876  
R;Chanut, F.A.  
Submitted to the EMBL Data Library, July 1992  
A;Reference number: S29873  
A;Accession: S29876  
A;Status: conceptual translation of pseudogene  
A;Molecule type: DNA  
A;Cross-references: EMBL:Z14032; GB:6553383; GB:6553390; GB:6553391; GB:6553457; NID:922

Query Match Score 40.2%; Best Local Similarity 42.3%; Pred. No. 8.8%;  
Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

Qy 1 DVLKKGTVLAHGGKAALGAVADT 25  
Db 88 DLVKKRTGSIVDPAGKMLGRVVDAL 113

RESULT 6

S33922 H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - sugar beet mitochondrial ATP synthase  
N;Alternate names: ATPase alpha chain  
C;Species: mitochondrial Beta vulgaris var. altissima (sugar beet)  
C;Accession: S33922  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 03-Jun-2002  
R;Sendai, M.; Mikami, T.; Kinoshita, T.  
Curr. Genet. 24, 164-170, 1993  
A;Title: The sugar beet mitochondrial gene for the ATPase alpha-subunit: sequence, transcription, and comparison with conceptual translation  
A;Reference number: S33922; MUID:9336527; PMID:8358823  
A;Accession: S33922  
A;Status: not compared with conceptual translation  
A;Molecule type: DNA  
A;Cross-references: GB:D15065; NID:9285631; PIDN:BAA03664\_1; PID:9285632  
A;Genome: mitochondrial  
C;Superfamily: H+-transporting ATP synthase alpha chain homology <ATP>  
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrial  
P;171-178/Region: nucleotide-binding motif A (P-loop)  
P;205-377/Domain: H+-transporting ATP synthase alpha chain homology <ATP>

Query Match Score 40.2%; Best Local Similarity 42.3%; Pred. No. 14%;  
Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

Qy 1 DVLKKGTVLAHGGKAALGAVADT 25  
Db 88 DLVKKRTGSIVDPAGKMLGRVVDAL 113

RESULT 7

S44508 H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - beet mitochondrial ATP synthase  
N;Alternate names: ATPase alpha chain  
C;Species: mitochondrial Beta vulgaris (beet)  
C;Date: 15-Jul-1995 #sequence\_revision 23-Feb-1996 #text\_change 03-Jun-2002  
C;Accession: S44508; S46507; S29535; S29536

Query Match	4.0-2%	Score 51.5;	DB 2;	Length 507;
Best Local Similarity	42.3%;	Pred. No. 14;		
Matches	11;	Conservative	7;	Mismatches 7; Indels 1; Gaps 1;
Qy	1 DVKKIGTVLAHAGKAALGAVADTI 25			
Db	88 DLVKRTGSIVDVPAKGAKLGRVVDAL 113			
RESULT 9				
A26760				
A+ transporting two-sector ATPase (EC 3.6.3.14) alpha chain - garden pea mitochondrial				
C;Species:	mitochondrion Pisum sativum (garden pea)			
C;Date:	09-May-1988 #sequence_revision 09-May-1988 #text_change 03-Jun-2002			
R;Morikami, A.; Nakamura, K.				
J. Biochem. 101, 967-976, 1987				
A;Title: Structure and expression of pea mitochondrial F1-ATPase alpha-subunit gene and				
A;Reference number: A26760; PMID:8727992; PMID:2886497				
A;Accession: A26760				
A;Status: preliminary; not compared with conceptual translation				
A;Molecule type: DNA				
A;Residues: 1-507 <MOR>				
C;Genetics:				
A;Genome: mitochondrial				
C;Superfamily: H+-transporting ATP synthase alpha-chain; H+-transporting ATP synthase a				
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; nu-				
C;Species: mitochondrial				
F;171-178:Region: nucleotide-binding motif A (P-loop)				
F;205-377:Domain: H+-transporting ATP synthase alpha chain homology <ATP>				
Query Match	4.0-2%	Score 51.5;	DB 2;	Length 507;
Best Local Similarity	42.3%;	Pred. No. 14;		
Matches	11;	Conservative	7;	Mismatches 7; Indels 1; Gaps 1;
Qy	1 DVKKIGTVLAHAGKAALGAVADTI 25			
Db	88 DLVKRTGSIVDVPAKGAKLGRVVDAL 113			
RESULT 10				
PWZMAM				
A+ transporting two-sector ATPase (EC 3.6.3.14) alpha chain - maize mitochondrial				
N;Alternative names: ATPase alpha chain				
C;Species: mitochondrial Zea mays (maize)				
C;Accession: A23757				
R;Braun, C.J.; Levings III, C.S.				
Plant Physiol. 79, 571-577, 1985				
A;Title: Nucleotide sequence of the F1-ATPase alpha subunit gene from maize mitochondrial				
A;Reference number: A23757				
A;Accession: A23757				
A;Molecule type: DNA				
A;Residues: 1-508 <BRA>				
C;Genetics:				
A;Gene: atpa				
A;Genome: mitochondrial				
C;Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase a				
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion; nu-				
C;Species: mitochondrial				
F;171-178:Region: nucleotide-binding motif A (P-loop)				
F;205-377:Domain: H+-transporting ATP synthase alpha chain homology <ATP>				
F;268-277:Region: nucleotide-binding motif B				
F;376/Active site: ATP (Lys) #status predicted				
Query Match	4.0-2%	Score 51.5;	DB 1;	Length 508;
Best Local Similarity	42.3%;	Pred. No. 14;		
Matches	11;	Conservative	7;	Mismatches 7; Indels 1; Gaps 1;
Qy	1 DVKKIGTVLAHAGKAALGAVADTI 25			
Db	88 DLVKRTGSIVDVPAKGAKLGRVVDAL 113			

Nucleic Acids Res. 17, 7531, 1989  
 A;Title: Wheat mitochondrial DNA: organization and sequence  
 A;Reference number: S06007; MUID:90016824; PMID:2529479  
 A;Accession: S05607  
 A;Status: translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-509 <SCH>  
 A;Cross-references: EMBL:X15918  
 C;Genetics:  
 A;Gene: atpa  
 A;Genome: mitochondrial  
 C;Superfamily: H+-transporting ATP synthase alpha chain;  
 C;Keywords: ATP biosynthesis; hydrolase; membrane-associated  
 C;Species: mitochondrial  
 C;Accession: P0171-178/Region: nucleotide-binding motif A (P-loop)  
 F:205-377/Domain: H+-transporting ATP synthase alpha chain  
 P:268-273/Region: nucleotide-binding motif B  
 P:177/Binding site: ATP (Lys) #status predicted  
 F:376/Active site: Arg #status predicted

Query	1 DVLLKIGTVA-LHAGKAALGAVADTI 25	Score 40.2*	DB 1;	Le
Best Local Similarity	40.23*	Score 51.5;	DB 1;	Le
Matches	11;	Pred. No. 14;		
Conservative	7;	Mismatches	7;	I

Db	88 DLVRKTGSIVDVYPAGKAMLGRVVDAL 113
----	------------------------------------

**RESULT 14**  
 PWZRZAM  
 H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain;  
 C;Species: mitochondrial Oryza sativa (rice)  
 C;Accession: J00411  
 C;Accession: K; Kazama, S.; Suzuki, T.  
 Nucleic Acids Res 18, 1302, 1990.  
 A;Title: Nucleotide sequence of the F1-ATPase alpha subunit  
 A;Reference number: J00411; MUID:90206808; PMID:2138730  
 A;Accession: J00411  
 A;Molecule type: DNA  
 A;Residues: 1-509 <SCH>  
 A;Cross-references: EMBL:X51422; NID:913958; PIDN:CAA357  
 C;Genetics:  
 A;Gene: atpa  
 A;Genome: mitochondrial  
 C;Superfamily: H+-transporting ATP synthase alpha chain;  
 C;Keywords: ATP biosynthesis; hydrolase; membrane-associated  
 C;Species: mitochondrial Helianthus annuus (common sunflower)  
 C;Accession: P0171-178/Region: nucleotide-binding motif A (P-loop)  
 F:205-377/Domain: H+-transporting ATP synthase alpha chain  
 P:268-273/Region: nucleotide-binding motif B  
 P:177/Binding site: ATP (Lys) #status predicted  
 F:376/Active site: Arg #status predicted

Query	1 DVLLKIGTVA-LHAGKAALGAVADTI 25	Score 40.2*	DB 1;	Le
Best Local Similarity	40.23*	Score 51.5;	DB 1;	Le
Matches	11;	Pred. No. 14;		
Conservative	7;	Mismatches	7;	I

Db	88 DLVRKTGSIVDVYPAGKAMLGRVVDAL 113
----	------------------------------------

**RESULT 15**  
 S10597  
 H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain;  
 C;Species: mitochondrial Helianthus annuus (common sunflower)  
 C;Accession: P0171-178/Region: nucleotide-binding motif A (P-loop)  
 C;Accession: S10597; S1074; S17799; S52010; S8854  
 C;Accession: R.H.; Roehler, R.H.; Loessel, A.; Zetsche, K.  
 Nucleic Acids Res 1, 4588, 1990.  
 A;Title: Nucleotide sequence of the F1-ATPase alpha subunit  
 A;Reference number: S10597; MUID:90356396; PMID:2143817  
 A;Accession: S10597  
 A;Molecule type: DNA  
 A;Residues: 1-509 <SCH>

Molecule type: DNA  
 Residues: 1-510 <KOB>  
 A; Cross-references: EMBL:X53537; NID:912577; PIDN:CHA37613.1; PID:9758362  
 A; Experimental source: Line Babo  
 R; Siciliana, L.; D'Ambrosio, L.; de Tuglie, A.D.; Gallerani, R.  
 Nucleic Acids Res. 18, 4599, 1990  
 A; Title: Minor differences in the primary structures of atpa genes coded on the mtDNA of  
 A; Reference number: S10974; MUID:90356407; PMID:2143818  
 A; Accession: S10974  
 A; Molecule type: DNA  
 A; Residues: 1-510 <SIC>  
 A; Cross-references: EMBL:X52838; NID:912988; PIDN:CAA37022.1; PID:912989  
 A; Experimental source: strain Ha89  
 R; Koehler, R.H.; Horn, R.; Loesel, A.; Zetsche, K.  
 Mol. Gen. Genet. 227, 369-376, 1991  
 A; Title: Cytoplasmic male sterility in sunflower is correlated with the co-transcription  
 A; Reference number: S16528; MUID:91326025; PMID:1714033  
 A; Accession: S17799  
 A; Status: translation not shown  
 A; Molecule type: DNA  
 A; Residues: 1-510 <KCA>  
 A; Cross-references: EMBL:X55963; NID:912985; PIDN:CAA39428.1; PID:912986  
 A; Experimental source: line CMBBabO  
 R; Spasibova, M.; Moneger, P.; Leaver, C.J.; Petrov, P.; Atanassov, A.; Nijkamp, H.J.J.; H  
 Plant Mol. Biol. 26, 1819-1831, 1994  
 A; Title: Characterisation and expression of the mitochondrial genome of a new type of cy  
 A; Reference number: S52010; MUID:95161706; PMID:7858220  
 A; Accession: S52010  
 A; Status: translation not shown  
 A; Molecule type: DNA  
 A; Residues: 293-510 <SPA>  
 A; Cross-references: EMBL:X823886; NID:9563544; PIDN:CAA57786.1; PID:9563545  
 C; Genetics:  
 A; Gene: atpa  
 A; Genome: mitochondrial  
 C; Superfamily: H+-transporting ATP synthase alpha chain  
 C; Key words: H+-transporting ATP synthase; hydrolase; membrane-associated complex; mitochondrion; nucleotide-binding motif A (P-loop)  
 P; 171-178 Region: nucleotide-binding motif A (P-loop)  
 F; 205-377 Domain: H+-transporting ATP synthase alpha chain homology <ATP>  
 Query Match Score 51.5; DB 2; Length 510;  
 Best Local Similarity 40.2%; Score 51.5; DB 2; Length 510;  
 Matches 11; Conservative 7; Mismatches 7; Indels 1; Gaps 1;  
 Qy 1 DWIKKGTVLA-HAGKRALGAVDTI 25  
 Db 88 DLVKRTSSIVDYPAGXAMLRVYDAL 113

Search completed: December 10, 2003, 20:29:27  
 Job time : 22 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 10, 2003, 20:27:46 ; Search time 30 Seconds  
 (without alignments)  
 167.385 Million cell updates/sec

Title: US-09-936-885-3

Perfect score: 128

Sequence: 1 DVULKIGTVHALGKAAALGAVADTISQ 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters:

Database : Published Applications AA: \*

```

1: /cgn2_6/_prodatal2/_pubpaas/us07_PUBCOMB.pep:*
2: /cgn2_6/_prodatal2/_pubpaas/FCT_NEW_PUB.pep:*
3: /cgn2_6/_prodatal2/_pubpaas/us06_NEW_PUB.pep:*
4: /cgn2_6/_prodatal2/_pubpaas/us05_PUBCOMB.pep:*
5: /cgn2_6/_prodatal2/_pubpaas/us07_NEW_PUB.pep:*
6: /cgn2_6/_prodatal2/_pubpaas/PECTUS_PUBCOMB.pep:*
7: /cgn2_6/_prodatal2/_pubpaas/us08_NEW_PUB.pep:*
8: /cgn2_6/_prodatal2/_pubpaas/us08_PUBCOMB.pep:*
9: /cgn2_6/_prodatal2/_pubpaas/us09A_PUBCOMB.pep:*
10: /cgn2_6/_prodatal2/_pubpaas/us09B_PUBCOMB.pep:*
11: /cgn2_6/_prodatal2/_pubpaas/us09C_PUBCOMB.pep:*
12: /cgn2_6/_prodatal2/_pubpaas/us09_NEW_PUB.pep:*
13: /cgn2_6/_prodatal2/_pubpaas/us10A_PUBCOMB.pep:*
14: /cgn2_6/_prodatal2/_pubpaas/us10B_PUBCOMB.pep:*
15: /cgn2_6/_prodatal2/_pubpaas/us10C_PUBCOMB.pep:*
16: /cgn2_6/_prodatal2/_pubpaas/us10_NEW_PUB.pep:*
17: /cgn2_6/_prodatal2/_pubpaas/us60_NEW_PUB.pep:*
18: /cgn2_6/_prodatal2/_pubpaas/us60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	128	100.0	31 14 US-10-038-045-13	Sequence 13, Appl
2	110	65.9	33 9 US-09-917-340-21	Sequence 21, Appl
3	110	65.9	33 11 US-09-908-139-23	Sequence 23, Appl
4	110	65.9	33 15 US-10-197-954-45	Sequence 45, Appl
5	105	65.9	34 14 US-10-038-045-7	Sequence 7, Appl
6	105	62.0	34 9 US-09-917-340-22	Sequence 22, Appl
7	105	82.0	34 14 US-10-038-045-8	Sequence 3, Appl
8	99.5	77.7	32 9 US-09-030-619-201	Sequence 20, Appl
9	73	57.0	19 14 US-10-038-045-16	Sequence 16, Appl
10	59	46.1	30 11 US-09-908-139-20	Sequence 20, Appl
11	55	43.0	18 14 US-10-038-045-11	Sequence 11, Appl
12	54	42.2	29 11 US-09-908-139-19	Sequence 19, Appl
13	54	42.2	29 11 US-09-908-139-21	Sequence 21, Appl
14	51.5	40.2	33 14 US-10-038-045-14	Sequence 14, Appl
15	49	38.3	287 9 US-09-864-761-42836	Sequence 42836, A

RESULT 1  
 US-10-038-045-13  
 ; Sequence 13, Application US-100380045  
 ; Publication No. US2002150964A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mor, Amram  
 ; Voudourakis, Ioannis  
 ; NICOLAS, Pierre  
 ; TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION  
 ; OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS  
 ; NUMBER OF SEQUENCES: 16  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds LLP  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: NY  
 ; COUNTRY: USA  
 ; ZIP: 10036-2811  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows  
 ; SOFTWARE: PASEQ for Windows Version 2.0b  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US-10/038,045  
 ; FILING DATE: 03-Jan-2002  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US-09/181,941  
 ; FILING DATE: 28-Oct-1998  
 ; APPLICATION NUMBER: US-08/574,701  
 ; FILING DATE: 19-DEC-1995  
 ; APPLICATION NUMBER: FR-95 07831  
 ; FILING DATE: 29-JUN-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Corruzi, Laura A.  
 ; REGISTRATION NUMBER: 30,742  
 ; REFERENCE/DOCKET NUMBER: 3909-0021-999

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-493-4935  
 TELEX: 650-93-5556  
 TELX: 66141 FENNIE  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 31 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: Single  
 TOPOLOGY: linear  
 MOLECULE TYPE: No. US20020150964A1e  
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-10-038-045-13

Query Match 100.0%; Score 128; DB 14; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-13;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 DVLKKGTVVALHAGKAALGAVADTISQ 27  
 Db 5 DVLKKGTVVALHAGKAALGAVADTISQ 31

RESULT 2  
 US-09-917-340-21  
 Sequence 21, Application US/09917340  
 Patent No. US20020090369A1  
 GENERAL INFORMATION:  
 APPLICANT: Murphy, Christopher J.  
 APPLICANT: McAnulty, Jonathan P.  
 APPLICANT: Reid, Ted W.  
 TITLE OF INVENTION: Transplant Media  
 FILE REFERENCE: PLANT-06468  
 CURRENT APPLICATION NUMBER: US/09/917,340  
 CURRENT FILING DATE: 2001-07-29  
 PRIOR APPLICATION NUMBER: 60/221,632  
 PRIOR FILING DATE: 2000-07-28  
 PRIOR APPLICATION NUMBER: 60/249,602  
 PRIOR FILING DATE: 2000-11-17  
 PRIOR APPLICATION NUMBER: 60/290,932  
 PRIOR FILING DATE: 2001-05-15  
 NUMBER OF SEQ ID NOS: 96  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO 21  
 LENGTH: 33  
 TYPE: PRT  
 ORGANISM: Phylomedusa sauvagei  
 US-09-917-340-21

Query Match 85.9%; Score 110; DB 9; Length 33;  
 Best Local Similarity 84.6%; Pred. No. 3.2e-10;  
 Matches 23; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 Qy 2 VLKKIGTVVALHAGKAALGAVADTISQ 27  
 Db 6 MLKKLGTMALHAGKAALGAAADTISQ 31

RESULT 3  
 US-09-908-139-23  
 Sequence 23, Application US/09908139  
 Publication No. US2003009649A1  
 GENERAL INFORMATION:  
 APPLICANT: Hancock, Robert B. W.  
 APPLICANT: Gough, Monisha A.  
 APPLICANT: Patryk, Kat, Aleksander  
 APPLICANT: Woods, Donald  
 APPLICANT: Jia, Xiaoyan  
 TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC PEPTIDES AND METHODS OF USE THEREFOR  
 FILE REFERENCE: 07422/016001  
 CURRENT APPLICATION NUMBER: US/09/908,139  
 CURRENT FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: 09/143,124  
 PRIOR FILING DATE: 1998-08-28  
 NUMBER OF SEQ ID NOS: 25  
 SOFTWARE: PastSEQ for Windows Version 4.0  
 SEQ ID NO 23  
 LENGTH: 33  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION: antimicrobial cationic peptide  
 US-09-908-139-23  
 Query Match 85.9%; Score 110; DB 11; Length 33;  
 Best Local Similarity 84.6%; Pred. No. 3.2e-10;  
 Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 Qy 2 VLKKIGTVVALHAGKAALGAVADTISQ 27  
 Db 6 MLKKLGTMALHAGKAALGAAADTISQ 31  
 RESULT 4  
 US-10-197-954-45  
 Sequence 45, Application US/10197954  
 Publication No. US20030119021A1  
 GENERAL INFORMATION:  
 APPLICANT: K'ster, Hubert  
 APPLICANT: Siddiqi, Suhaib  
 APPLICANT: Little, Daniel  
 TITLE OF INVENTION: Capture Compounds, Collections Thereof And Methods For Analyzing The Proteome And Complex  
 TITLE OF INVENTION: Compositions  
 FILE REFERENCE: 24743-2305  
 CURRENT APPLICATION NUMBER: US/10/197,954  
 CURRENT FILING DATE: 2002-07-16  
 PRIOR APPLICATION NUMBER: 60/306,019  
 PRIOR FILING DATE: 2001-07-16  
 PRIOR APPLICATION NUMBER: 60/314,123  
 PRIOR FILING DATE: 2001-08-21  
 PRIOR APPLICATION NUMBER: 60/363,433  
 PRIOR FILING DATE: 2002-03-11  
 NUMBER OF SEQ ID NOS: 149  
 SOFTWARE: PastSEQ for Windows Version 4.0  
 SEQ ID NO 45  
 LENGTH: 33  
 TYPE: PRT  
 ORGANISM: Homo Sapiens  
 US-10-197-954-45  
 Query Match 85.9%; Score 110; DB 15; Length 33;  
 Best Local Similarity 84.6%; Pred. No. 3.2e-10;  
 Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 Qy 2 VLKKIGTVVALHAGKAALGAVADTISQ 27  
 Db 6 MLKKLGTMALHAGKAALGAAADTISQ 31  
 RESULT 5  
 US-10-038-045-7  
 Sequence 7, Application US/10038045  
 Publication No. US20020150964A1  
 GENERAL INFORMATION:  
 APPLICANT: Mor, Amram  
 APPLICANT: Vouloudakis, Ioannis  
 APPLICANT: Nicolas, Pierre  
 TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION  
 OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds LLP  
 STREET: 115 Avenue of the Americas  
 CITY: New York

```

STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows Version 2.0b
SOFTWARE: FASTSEQ for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/038,045
FILING DATE: 02-Jan-2002
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/181,941
FILING DATE: 28-OCT-1998
APPLICATION NUMBER: US/08/574,701
FILING DATE: 19-DEC-1995
APPLICATION NUMBER: PR 95 07831
FILING DATE: 29-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 0,742
REFERENCE DOCKET NUMBER: 3909-0021-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 65141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No.
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-038-045-7

Query Match          Score 110,  DB 14; Len 6
Best Local Similarity 84.6%; Pred. No. 3.4e-10;
Matches 22; Conservative 3; Mismatches 1, In
Qy   2 VLIKKGITVALHAGKAALGAVADISQ 27
Db   6 MLKKGITVALHAGKAALGAVADISQ 31

RESULT 6
US-09-917-340-22
Sequence 22, Application US/09917340
PATENT INFORMATION:
FILED REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,502
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver: 2.0
SEQ ID NO 22
LENGTH: 34
TYPE: PRT
ORGANISM: Phyllomedusa sauvagei

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Best Local Similarity 80.8%; Pred. No. 2e-09; Matches 21; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Query 2 VLIKKGTVHALGKAAALGAVADTISQ 27  
Db 6 MLKKGTMALHAGKAAALGAAANTISQ 31

RESULT 7

US-10-038-045-8

Sequence 8, Application US/10038045  
Publication No. US2002150964A1

GENERAL INFORMATION:

APPLICANT: Mor Amram  
Vouldoukis, Ioannis

TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS

NUMBER OF SEQUENCES: 16.

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/038, 045  
FILING DATE: 02-Jan-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/181, 941  
FILING DATE: 28-Oct-1998  
APPLICATION NUMBER: US/08/574, 701  
FILING DATE: 19-DEC-1995  
APPLICATION NUMBER: FR 95 07831  
FILING DATE: 29-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Cornuzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 3909-0021-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-4355  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: No. US2002150964A1  
SEQUENCE DESCRIPTION: SEQ ID NO: 8;  
US-10-038-045-8

Query Match 82.0%; Score 105; DB 14; Length 34;  
Best Local Similarity 80.8%; Pred. No. 2e-09; Matches 21; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Query 2 VLIKKGTVHALGKAAALGAVADTISQ 27  
Db 6 MLKKGTMALHAGKAAALGAAANTISQ 31

RESULT 8

GENERAL INFORMATION:

APPLICANT: Krieger, Timothy J.

APPLICANT: Taylor, Robert

APPLICANT: Erflie, Douglas S.

APPLICANT: Fraser, Janet R.

APPLICANT: Weitz, Michael H.D.

APPLICANT: McNicol, Patricia J.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING TIME OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION WITH ANTIBIOTICS

FILE REFERENCE: 660081.406

CURRENT APPLICATION NUMBER: US/09/030,619B

CURRENT FILING DATE: 1998-02-25.

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 232

TYPE: PRT

ORGANISM: Phylomedusa sauvagii

US-09-030-619-201

RESULT 9  
Query Match 77.7%; Score 99.5; DB 9; Length 32;  
Best Local Similarity 84.6%; Pred. No. 1 4e-08;  
Matches 22; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

Qy 2 VIKKIGTVVALHAGKALGAVADTISQ 27  
Db 6 MLRKCLTMALHAGKALGAVADTISQ 30

GENERAL INFORMATION:

APPLICANT: Mor, Amram

ADDRESSEE: Vouldoukis, Ioannis B

Nicolas, Pierre

Vouldoukis, Ioannis B

TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Penne & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

ZIP: 10036-2811

COMPUTER READABLE FORM:

COMPILER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/038,045

FILING DATE: 02-Jan-2002

PRIOR APPLICATION DATA:

CLASSIFICATION: <Unknown>

APPLICATION NUMBER: US/09/181,941

FILING DATE: 28-Oct-1998

APPLICATION NUMBER: US 08/574,701

FILING DATE: 19-DEC-1995

APPLICATION NUMBER: FR 95 07831

FILING DATE: 29-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE DOCKET NUMBER: 3909-0021-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-9355

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-10-038-045-16

Query Match 57.0%; Score 73; DB 14; Length 19;  
Best Local Similarity 93.8%; Pred. No. 0.00011;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 PRGKAALGAVADTISQ 27  
Db 1 PRGKAALGAVADTISQ 16

RESULT 10  
US-09-908-139-20  
Sequence 20, Application US/09908139  
Publication No. US200301096949A1

GENERAL INFORMATION:

APPLICANT: Hancock, Robert E. W.

APPLICANT: Gough, Monisha A.

APPLICANT: Patryk, Aleksander

APPLICANT: Woods, Donald

APPLICANT: Xiaoyan, Jia

TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC PEPTIDES AND METHODS OF USE THEREFOR

CURRENT APPLICATION NUMBER: US/09/908,139

FILE REFERENCE: 07422/016001

CURRENT FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: 09/143,124

PRIOR FILING DATE: 1998-08-28

NUMBER OF SEQ ID NOS: 25

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 20

LENGTH: 30

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: antimicrobial cationic peptide

US-09-908-139-20

Query Match 46.1%; Score 59; DB 11; Length 30;  
Best Local Similarity 61.9%; Pred. No. 0.0281;  
Matches 13; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 2 VIKKIGTVVALHAGKALGAVA 22  
Db 6 MLRKCLTMALHAGKALGAV 26

RESULT 11  
US-10-038-045-11

Sequence 11, Application US/10038045

Publication No. US20020150964A1

GENERAL INFORMATION:

APPLICANT: Mor, Amram

Vouldoukis, Ioannis B

Nicolas, Pierre

TITLE OF INVENTION: PEPTIDS FOR THE ACTIVATION OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Penne & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

ZIP: 10036-2811

COMPUTER READABLE FORM:

COMPILER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/038,045

FILING DATE: 02-Jan-2002

PRIOR APPLICATION DATA:

CLASSIFICATION: <Unknown>

APPLICATION NUMBER: US/09/181,941

FILING DATE: 28-Oct-1998

APPLICATION NUMBER: US 08/574,701

FILING DATE: 19-DEC-1995

APPLICATION NUMBER: FR 95 07831

FILING DATE: 29-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE DOCKET NUMBER: 3909-0021-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-9355

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 16:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows  
 SOFTWARE: FastSEQ for Windows Version 2.0b  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/038, 045  
 FILING DATE: 02-Jan-2002  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/181, 941  
 FILING DATE: 28-Oct-1998  
 APPLICATION NUMBER: US/08/574, 701  
 FILING DATE: 19-DEC-1995  
 APPLICATION NUMBER: FR 95 07831  
 FILING DATE: 29-JUN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 3909-0021-999  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-493-4935  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 amino acids  
 TYPE: Amino Acid  
 STRANDEDNESS: Single  
 TOPOLOGY: Linear  
 MOLECULE TYPE: No. US2002015064A1  
 SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
 /US-10-038-045-11

Query Match 43.0%; Score 55; DB 14; Length 18;  
 Best Local Similarity 76.9%; Pred. No. 0.065;  
 Matches 10; Conservative 3; Mismatches 0; Indels 0;  
 Gaps 0;

Qy 2 VLKIGTVLHAG 14  
 Db 6 MLKKGTMALHAG 18

RESULT 12

US-09-908-139-19  
 Sequence 19, Application US/09908139  
 Publication No. US20030096349A1  
 GENERAL INFORMATION:  
 / APPLICANT: Hancock, Robert E. W.  
 / APPLICANT: Gough, Monisha A.  
 / APPLICANT: Patryk, Aleksander  
 / APPLICANT: Woods, Donald  
 / TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC  
 / PEPTIDES AND METHODS OF USE THEREFOR  
 / FILE REFERENCE: 0742/016001  
 / CURRENT APPLICATION NUMBER: US/09/908,139  
 / PRIOR APPLICATION NUMBER: 09/143,124  
 / PRIOR FILING DATE: 1998-08-28  
 / LENGTH: 29  
 / TYPE: PRT  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: antimicrobial cationic peptide

Query Match 42.2%; Score 54; DB 11; Length 29;  
 Best Local Similarity 63.2%; Pred. No. 0.16;  
 Matches 12; Conservative 0; Mismatches 7; Indels 0;  
 Gaps 0;

Qy 4 KKIGTVLHAGKAALGAVA 22  
 /US-09-908-139-19

RESULT 14

US-10-038-045-14  
 Sequence 14, Application US/10038045  
 Publication No. US2003150964A1  
 GENERAL INFORMATION:  
 / APPLICANT: Voudouris, Ioannis  
 / APPLICANT: Nicolas, Pierre  
 / TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION  
 / OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS  
 / NUMBER OF SEQUENCES: 16  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Pennie & Edmonds LLP  
 / STREET: 115 Avenue of the Americas  
 / CITY: New York  
 / STATE: NY  
 / ZIP: 10016-2811  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Diskette  
 / COMPUTER: IBM Compatible  
 / OPERATING SYSTEM: Windows  
 / SOFTWARE: FastSEQ for Windows Version 2.0b  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/10/038, 045  
 / FILING DATE: 02-Jan-2002  
 / CLASSIFICATION: <Unknown>  
 / PRIORITY APPLICATION DATA:  
 / APPLICATION NUMBER: US/09/181, 941  
 / FILING DATE: 28-Oct-1998  
 / APPLICATION NUMBER: US 08/574, 701  
 / FILING DATE: 19-Dec-1995  
 / APPLICATION NUMBER: FR 95 07831

Qy 4 KKIGTVLHAGKAALGAVA 22

FILING DATE: 29-JUN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: CORUZZI, Laura A  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 3909-0021-999  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-493-4935  
 TELEX: 66141 PENNIE  
 TELEFAX: 650-493-5556  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 33 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: No. US20020150964A1  
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
 US-10-038-005-14

Query Match Score 51.5; DB 14; Length 33;  
 Best Local Similarity 42.9%; Pred. No. 0.46%;  
 Matches 12; Conservative 6; Mismatches 5; Indels 5; Gaps 1;

Qy 3 LKKIG---TVLHAGKQALGAVADTI 25  
 : : : | | | | | | | | | | : : :  
 Db 6 IREVGEAKAAKAAGAAKGAAALGAVSEAV 33

RESULT 15  
 US-09-864-761-42836  
 ; Sequence 42836, Application US/09864761  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wenshieng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; FILE REFERENCE: Aeomics-X-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; PRIOR FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60,180,312  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: US 60,207,456  
 ; PRIOR FILING DATE: 2000-05-16  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: GB 24663,6  
 ; PRIOR FILING DATE: 2000-10-04  
 ; PRIOR APPLICATION NUMBER: US 60,236,359  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: US 60,234,687

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PRIOR FILING DATE: 2000-09-21  
 ; PRIOR APPLICATION NUMBER: US 09/608,408  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: US 09/774,203  
 ; PRIOR FILING DATE: 2001-01-29  
 ; NUMBER OF SEQ ID NOS:  
 ; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
 ; SEQ ID NO: 42836  
 ; LENGTH: 287  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: MAP TO AL049870.1  
 ; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.6  
 ; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7  
 ; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.2  
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96  
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.98  
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.98  
 ; OTHER INFORMATION: EST HUMAN HIT: U69560\_1, EVALUATE 3.00e-55  
 ; OTHER INFORMATION: SWISSPROT HIT: Q04652, EVALUATE 3.00e-57  
 ; US-09-864-761-42836

Query Match Score 49; DB 9; Length 287;  
 Best Local Similarity 36.4%; Pred. No. 14%;  
 Matches 8; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 1 DVLLKIGTVHALGAKALGAVA 22  
 : : : | | | | | | | | : : :  
 Db 36 DILLRVGDVKIHAKVYLASVS 57

Search completed: December 10, 2003, 20:30:44  
 Job time : 30 SECs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: December 10, 2003, 20:26:51 ; Search time 21 seconds

(without alignments)  
 54 400 Million cell updates/sec

Title: US-09-936-885-3

Perfect score: 128

Sequence: 1 DVLLKIGTVLHAGKAAGAVADTISQ 27

Scoring table: BLOSUM62

Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA;

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  2: /cgn2_6/picodata/1/1aa/5B-COMB.PEP:*
  3: /cgn2_6/picodata/1/1aa/6A-COMB.PEP:*
  4: /cgn2_6/picodata/1/1aa/6B-COMB.PEP:*
  5: /cgn2_6/picodata/1/1aa/PCFTIS-COMB.PEP:*
  6: /cgn2_6/picodata/1/1aa/backfile11.PEP:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description	
1	128	100.0	31	4	US-09-181-941-13		Sequence 13, APP1	
2	110	85.9	33	3	US-09-143-124-23		Sequence 23, APP1	
3	110	85.9	34	4	US-09-181-941-7		Sequence 7, APP1	
4	105	82.0	34	4	US-09-181-941-8		Sequence 8, APP1	
5	99.5	77.7	32	4	US-09-030-619-201		Sequence 201, APP1	
6	73	57.0	19	4	US-09-181-941-16		Sequence 16, APP1	
7	7	59	46.1	30	3	US-09-143-124-20		Sequence 20, APP1
8	55	43.0	18	4	US-09-181-941-11		Sequence 11, APP1	
9	54	42.2	29	3	US-09-143-124-19		Sequence 19, APP1	
10	54	42.2	29	3	US-09-143-124-21		Sequence 21, APP1	
11	51.1	40.2	33	4	US-09-181-941-14		Sequence 14, APP1	
12	49	38.3	265	4	US-09-052-991A-24310		Sequence 24310, APP1	
13	48.5	37.9	30	4	US-09-181-941-9		Sequence 9, APP1	
14	48	37.5	1209	5	PCT-US95-01595-107		Sequence 107, APP1	
15	48	37.5	1258	2	US-08-110-912A-107		Sequence 107, APP1	
16	48	37.5	1258	3	US-09-301-085-107		Sequence 107, APP1	
17	48	37.5	1294	3	US-8-930-99A-10-		Sequence 10, APP1	
18	45.5	35.5	625	4	US-09-052-991A-23005		Sequence 23005, APP1	
19	45	35.2	26	3	US-09-143-124-17		Sequence 17, APP1	
20	45	35.2	97	4	US-09-398-395A-40		Sequence 107, APP1	
21	45	35.2	97	4	US-09-387-586A-40		Sequence 40, APP1	
22	45	35.2	97	4	US-09-895-752-40		Sequence 40, APP1	
23	45	35.2	97	4	US-09-903-01-B-40		Sequence 40, APP1	
24	45	35.2	926	4	US-09-252-991A-1053		Sequence 31053, APP1	
25	44	34.4	29	3	US-09-143-124-24		Sequence 24, APP1	
26	44	34.4	1039	4	US-09-252-991A-24966		Sequence 28966, APP1	
27	43.5	34.0	566	4	US-09-252-991A-24498		Sequence 24498, APP1	

## ALIGNMENTS

RESULT 1  
 US-09-181-941-13  
 / Sequence 13, Application US/09181941  
 / Patent No. 6140690  
 / GENERAL INFORMATION:  
 / APPLICANT: Mor, Amram  
 / Voulioudakis, Ioannis  
 / NICOLAS, Pierre  
 / TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION  
 / OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS  
 / NUMBER OF SEQUENCES: 16  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Pennie & Edmonds LLP  
 / STREET: 1155 Avenue of the Americas  
 / CITY: New York  
 / STATE: NY  
 / COUNTRY: USA  
 / ZIP: 10036-2811  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Diskette  
 / COMPUTER: IBM Compatible  
 / OPERATING SYSTEM: Windows  
 / SOFTWARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/09/181-941  
 / FILING DATE: 28-OCT-1998  
 / CLASSIFICATION: Unknown>  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: US 08/574/701  
 / FILING DATE: 19-DEC-1995  
 / APPLICATION NUMBER: FR 95 07831  
 / FILING DATE: 29-JUN-1995  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Coruzzi, Laura A  
 / REGISTRATION NUMBER: 30,742  
 / REFERENCE/DOCKET NUMBER: 3909-0021-999  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: 650-493-4935  
 / TELEFAX: 650-493-5556  
 / TELEX: 6141 PENNIB  
 / INFORMATION FOR SEQ ID NO: 13:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 31 amino acids  
 / TYPE: amino acid  
 / STRANDEDNESS: Single  
 / TOPOLOGY: Linear  
 / MOLECULE TYPE: No. 6440690e  
 / SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
 / US-09-181-941-13

Query Match Simillarity 100.0%; Score 128; DB 4; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-14;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVLKIGTVLHAGKALGAVADTISQ 27  
 Db 5 DVLKIGTVLHAGKALGAVADTISQ 31

RESULT 2  
 US-09-143-124-23  
 Sequence 23, Application US/09143124  
 Patent No. 6288212  
 GENERAL INFORMATION:  
 APPLICANT: Hancock, Robert E. W.  
 APPLICANT: Gough, Monisha A.  
 APPLICANT: Patrzakat, Aleksander  
 APPLICANT: Woods, Donald  
 APPLICANT: Jia, Xiaoyan  
 TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC  
 PEPTIDES AND METHODS OF USE THEREFOR  
 FILE REFERENCE: 07422/016001  
 CURRENT APPLICATION NUMBER: US/09/143,124  
 CURRENT FILING DATE: 1998-08-28  
 NUMBER OF SEQ ID NOS: 25  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 23  
 LENGTH: 33  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURES:  
 OTHER INFORMATION: antimicrobial cationic peptide  
 US-09-143-124-23

Query Match Simillarity 85.9%; Score 110; DB 3; Length 33;  
 Best Local Similarity 84.6%; Pred. No. 5.7e-11;  
 Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VLKKIGTVLHAGKALGAVADTISQ 27  
 Db 6 MLKKGTMALHAGKALGAAADTISQ 31

RESULT 3  
 US-09-181-941-7  
 Sequence 7, Application US/09181941  
 Patent No. 6440690  
 GENERAL INFORMATION:  
 APPLICANT: Mor, Amram  
 Vouldoukis, Ioannis B  
 Nicolas, Pierre

TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: NY  
 ZIP: 10016-2811  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows  
 SOFTWARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/181,941  
 FILING DATE: 28-Oct-1998  
 CLASSIFICATION: <Unknown>  
 PRIORITY NUMBER: US/09/181,941  
 FILING DATE: 28-Oct-1998  
 PRIORITY NUMBER: <Unknown>  
 PRIORITY NUMBER: US/08/574,701  
 FILING DATE: 19-DEC-1995  
 PRIORITY NUMBER: US/08/574,701  
 FILING DATE: 29-JUN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 3909-0021-999  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-493-4935  
 TELEFAX: 650-493-5556  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 34 amino acids  
 TYPE: amino acid

APPLICATION NUMBER: FR 95 07831  
 FILING DATE: 29-JUN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 3909-0021-999  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-493-4935  
 TELEFAX: 650-493-5556  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 34 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: No. 6440690  
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
 US-09-181-941-7

Query Match Simillarity 85.9%; Score 110; DB 4; Length 34;  
 Best Local Similarity 84.6%; Pred. No. 5.9e-11;  
 Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VLKKIGTVLHAGKALGAVADTISQ 27  
 Db 6 MLKKGTMALHAGKALGAAADTISQ 31

RESULT 4  
 US-09-181-941-8  
 Sequence 8, Application US/09181941  
 Patent No. 6440690  
 GENERAL INFORMATION:  
 APPLICANT: Mor, Amram  
 Vouldoukis, Ioannis B  
 Nicolas, Pierre

TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: NY  
 ZIP: 10016-2811  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows  
 SOFTWARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/181,941  
 FILING DATE: 28-Oct-1998  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/08/574,701  
 FILING DATE: 19-DEC-1995  
 PRIORITY NUMBER: FR 95 07831  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A  
 REGISTRATION NUMBER: 30,742  
 REFERENCE/DOCKET NUMBER: 3909-0021-999  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-493-4935  
 TELEFAX: 650-493-5556  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 34 amino acids  
 TYPE: amino acid

STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: No. 6440690e  
 SEQUENCE DESCRIPTION: SEQ ID NO: 8  
 US-09-181-941-8

Query Match Score 105; DB 4; Length 34;  
 Best Local Similarity 80.8%; Pred. No. 3.7e-10;  
 Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLIKKGTVHALHAGKALGAVADTISQ 27  
 Db 6 MLKKGTVHALHAGKALGAVADTISQ 31

RESULT 5  
 US-09-030-619-201  
 Sequence 201, Application US/09030619B  
 Patent No. 6503881  
 GENERAL INFORMATION:  
 APPLICANT: Krieger, Timothy J.  
 APPLICANT: Taylor, Robert  
 APPLICANT: Brifley, Douglas  
 APPLICANT: Praser, Michael H.P.  
 APPLICANT: West, Janet R.  
 APPLICANT: McNicol, Patricia J.  
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING  
 TITLE OF INVENTION: COMPOSITIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION  
 WITH ANTIBIOTICS  
 FILE REFERENCE: 660081.406  
 CURRENT APPLICATION NUMBER: US/09/030,619B  
 CURRENT FILING DATE: 1998-02-25  
 NUMBER OF SEQ ID NOS: 232  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO 201  
 LENGTH: 32  
 TYPE: PRT  
 ORGANISM: Phylomedusa sauvagii

US-09-030-619-201

Query Match Score 99.5; DB 4; Length 32;  
 Best Local Similarity 84.6%; Pred. No. 2.6e-09;  
 Matches 22; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

Qy 2 VLIKKGTVHALHAGKALGAVADTISQ 27  
 Db 6 MLKKGTVHALHAGKALGAVADTISQ 30

RESULT 6  
 US-09-181-941-16  
 Sequence 16, Application US/09181941  
 Patent No. 6440690  
 GENERAL INFORMATION:  
 ADDRESSEE: Mor, Amram  
 APPLICANT: Vouloudakis, Ioannis  
 Nicolas, Pierre  
 INVENTION: PEPTIDES FOR THE ACTIVATION  
 OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS

NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 STREET: 115 Avenue of the Americas  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10036-2811  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows  
 SOFTWARE: FastSEQ for Windows Version 2.0b  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/181,941  
 FILING DATE: 28-Oct-1998  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/574,701  
 FILING DATE: 19-DEC-1995  
 APPLICATION NUMBER: PR 95 07831  
 FILING DATE: 29-JUN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Cortuzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-493-4935  
 TELEX: 650-493-5556  
 INFORMATION FOR SEQ ID NO: 16;  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 19 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
 US-09-181-941-16

Query Match Score 73; DB 4; Length 19;  
 Best Local Similarity 93.8%; Pred. No. 2.5e-05;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 HAGKALGAVADTISQ 27  
 Db 1 HAGKALGAVADTISQ 16

RESULT 7  
 US-09-143-124-20  
 Sequence 20, Application US/09143124  
 Patent No. 6288212  
 GENERAL INFORMATION:  
 APPLICANT: Hancock, Robert E. W.  
 APPLICANT: Gough, Monisha A.  
 APPLICANT: Patrykak, Aleksander  
 APPLICANT: Woods, Donald  
 APPLICANT: Jia, Xiaoyan  
 TITLE OF INVENTION: ANTI-ENDOTOXIN, ANTIMICROBIAL CATIONIC  
 PEPTIDES AND METHODS OF USE THEREFOR  
 FILE REFERENCE: 0742/016001  
 CURRENT APPLICATION NUMBER: US/09/143,124  
 CURRENT FILING DATE: 1998-08-28  
 NUMBER OF SEQ ID NOS: 25  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 20  
 LENGTH: 30  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: antimicrobial cationic peptide

US-09-143-124-20

Query Match Score 59; DB 3; Length 30;  
 Best Local Similarity 61.9%; Pred. No. 0.0074;  
 Matches 13; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 2 VLKKIGTVHALHAGKALGAV 22  
 Db 6 MLKKAHVGRHVGAALGAA 26

RESULT 8  
 US-09-181-941-11  
 Sequence 11, Application US/09181941  
 Patent No. 6440690  
 GENERAL INFORMATION:

APPLICANT: Mor, Amram  
Vouldoukis, Ioannis B.

TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION

NUMBER OF SEQUENCES: 16  
OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-3811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/181,941

FILING DATE: 28-Oct-1998

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/574,701

FILING DATE: 19-DEC-1995

PRIORITY NUMBER: FR 95 07831

FILING DATE: 29-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 3909-0021-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-4935

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6140690e

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-181-941-11

Query Match

Score 55; DB 4; Length 18;

Best Local Similarity 76.9%; Pred. No. 0.018;

Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLKKIGVALHAG 14

Db 6 MLKKIGTMLAHG 18

RESULT 9

Sequence 19, Application US/09143124

Patent No. 6288212

GENERAL INFORMATION:

APPLICANT: Hancock, Robert E. W.

APPLICANT: Gough, Monisha A.

APPLICANT: Patryyat, Aleksander

APPLICANT: Woods, Donald

APPLICANT: Jia, Xiaoyan

TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC

PEPTIDES AND METHODS OF USE THEREFOR

FILE REFERENCE: 07422/016001

CURRENT APPLICATION NUMBER: US/09/143,124

CURRENT FILING DATE: 1998-08-28

NUMBER OF SEQ ID NOS: 25

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 21

LENGTH: 29

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: antimicrobial cationic peptide

US-09-143-124-21

Query Match

Score 54; DB 3; Length 29;

Best Local Similarity 63.2%; Pred. No. 0.045;

Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4 KXIGTVLHAGKALGAVA 22

Db 7 KKAHHYGVTKVKGKALGAAA 25

RESULT 10

Sequence 21, Application US/09143124

Patent No. 6288212

GENERAL INFORMATION:

APPLICANT: Hancock, Robert E. W.

APPLICANT: Gough, Monisha A.

APPLICANT: Patryyat, Aleksander

APPLICANT: Woods, Donald

APPLICANT: Jia, Xiaoyan

TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC

PEPTIDES AND METHODS OF USE THEREFOR

FILE REFERENCE: 07422/016001

CURRENT APPLICATION NUMBER: US/09/143,124

CURRENT FILING DATE: 1998-08-28

NUMBER OF SEQ ID NOS: 25

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 29

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: antimicrobial cationic peptide

US-09-143-124-21

Query Match

Score 54; DB 3; Length 29;

Best Local Similarity 63.2%; Pred. No. 0.045;

Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4 KXIGTVLHAGKALGAVA 22

Db 7 KKAHHYGVTKVKGKALGAAA 25

RESULT 11

Sequence 14, Application US/09181941

Patent No. 6440650

GENERAL INFORMATION:

APPLICANT: Mor, Anram

APPLICANT: Vouldoukis, Ioannis B.

APPLICANT: Nicolas, Pierre

APPLICANT: Poulin, Pennie

APPLICANT: Edmonds, L.P.

TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION

OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 115 Avenue of the Americas

CITY: New York

STATE: NY

ZIP: 10016-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/181,941  
 FILING DATE: 28-Oct-1998  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/574,701  
 FILING DATE: 19-DEC-1995  
 APPLICATION NUMBER: FR 95 07831  
 FILING DATE: 29-JUN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Coruzzi, Laura A.  
 REGISTRATION NUMBER: 30,742  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-493-4935  
 TELEFAX: 650-493-5556  
 TEDEX: 66141 PENNIB  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 33 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: NO. 6440690E  
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
 US-09-181-941-14

Query Match Best Local Similarity 40.2%; Score 51.5; DB 4; Length 33;  
 Matches 12; Conservative 6; Mismatches 5; Indels 5; Gaps 1;

Qy 3 LKKIG-----TVLHAGKAALGAVADTI 25  
 Db 6 IREVGKEAAKAAKAAGKAAGLAVSEAV 33

RESULT 12  
 US-09-252-991A-24310  
 / Sequence 24310 Application US/09252991A  
 / Patent No. 6551795  
 / GENERAL INFORMATION:  
 / APPLICANT: Marc J. Rubenstein et al.  
 / TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 / TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 / FILE REFERENCE: 107196-136  
 / CURRENT APPLICATION NUMBER: US/09/252,991A  
 / CURRENT FILING DATE: 1999-02-18  
 / PRIOR APPLICATION NUMBER: US 60/074,788  
 / PRIOR FILING DATE: 1998-02-18  
 / PRIOR APPLICATION NUMBER: US 60/094,190  
 / PRIOR FILING DATE: 1998-07-27  
 / NUMBER OF SEQ ID NOS: 33142  
 / SEQ ID NO 24310  
 / LENGTH: 265  
 / TYPE: PRT  
 / ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-24310

Query Match Best Local Similarity 37.5%; Score 49; DB 4; Length 265;  
 Matches 12; Conservative 5; Mismatches 5; Indels 10; Gaps 1;

Qy 6 IGVVALH-----AGKAAALGAVADTISQ 27  
 Db 228 LGSVVLAHWPRDDCVERRRRLGTLADTIVSQ 259

RESULT 13  
 US-09-181-941-9  
 / Sequence 9 Application US/09181941  
 / Patent No. 6440690  
 / GENERAL INFORMATION:  
 / APPLICANT: Mor, Amram  
 / APPLICANT: Voudoukis, Ioannis

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30B  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/04589  
 FILING DATE:

CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/227,360  
 FILING DATE: 13-APR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Clark, Paul T.  
 REGISTRATION NUMBER: 30,162  
 REFERENCE DOCKET NUMBER: 00786/2300001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 542-5070  
 TELEX: (617) 542-8906  
 TELEFAX: (617) 542-8906  
 TELEX: 100254  
 INFORMATION FOR SEQ ID NO: 107:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1209 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US95-04589-107

Query Match 37.5%; Score 48; DB 5; Length 1209;  
 Best Local Similarity 46.4%; Pred. No. 32;  
 Matches 13; Conservative 4; Mismatches 9; Indels 2; Gaps 2;  
 Qy 1 DVLKKGTV-ALHAGK-AALGAVADTIS 26  
 Db 142 DALKKVGDLLKWHIGRNDKQGAIADKVS 169

\* RESULT 15  
 US-08-310-912A-107

Sequence 107, Application US/08310912A

Patent No. 5,981,730

GENERAL INFORMATION:

APPLICANT: Ausubel, Frederick M.  
 APPLICANT: Stratakis, Brian J.  
 APPLICANT: Brent, Andrew F.  
 APPLICANT: Dahlbeck, Douglas  
 APPLICANT: Karagiri, Fumiaki  
 APPLICANT: Kunkel, Barbara N.  
 APPLICANT: Mindrinos, Michael N.  
 APPLICANT: Yu, Guo-Liang

TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION  
 NUMBER OF SEQUENCES: 208  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEES: Fish & Richardson P.C.,  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2904

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30B

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/310,912A

FILING DATE: September 22, 1994

CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/227,360

FILING DATE: April 13, 1994

GenCore version 5.1.6  
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## OM protein - protein search, using SW model

Run on:

December 10, 2003, 20:24:16 ; Search time 42 Seconds  
 (without alignments)

102,039 Million cell updates/sec

Title: US-09-936-885-3  
 Perfect score: 128

Sequence: DVVKKIGTVLHAGKAALGAVADTISQ 27

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneset\_19gen03;\*

- 1: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA1980.DAT;\*
- 2: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA1981.DAT;\*
- 3: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA1982.DAT;\*
- 4: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA1983.DAT;\*
- 5: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA1984.DAT;\*
- 6: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA1985.DAT;\*
- 7: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA1986.DAT;\*
- 8: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA1987.DAT;\*
- 9: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA1988.DAT;\*
- 10: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA1989.DAT;\*
- 11: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA1990.DAT;\*
- 12: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA1991.DAT;\*
- 13: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA1992.DAT;\*
- 14: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA1993.DAT;\*
- 15: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA1994.DAT;\*
- 16: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA1995.DAT;\*
- 17: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA1996.DAT;\*
- 18: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA1997.DAT;\*
- 19: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA1998.DAT;\*
- 20: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA1999.DAT;\*
- 21: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA2000.DAT;\*
- 22: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA2001.DAT;\*
- 23: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA2002.DAT;\*
- 24: /SIDSI1/gcddata/geneseq/geneseqp-emb1/AA2003.DAT;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	128	100.0	27	21	AAB18725
2	128	100.0	31	21	AAB18726
3	128	100.0	31	21	AAB1436
4	128	100.0	32	21	AAB18748
5	128	100.0	78	21	AAB18724
6	110	85.9	33	21	AAY87380
7	110	85.9	33	21	AAU90985
8	110	83.9	34	21	AAB18732
9	110	85.9	34	22	AAB91864

Frog dermaseptin P	34	24	AAB34434
Amino acid sequenc	34	21	AAB18733
Transplant media a	34	23	AAU90986
Cationic peptide a	32	19	AAW6436
Cationic peptide d	32	21	AAY91737
Cationic peptide D	32	24	ABU59614
Cationic cancer t	30	21	AAY7377
Cationic antimicro	417	16	AAR66223
Cystathione gamma	29	21	AAV87376
Cationic antimicro	29	21	AAY87378
Cationic antimicro	31	21	AAB18738
Amino acid sequenc	30	21	AAB18731
Amino acid sequenc	30	21	AAB18711
Human liver peptid	287	22	ABB29733
Peptide #2344 enco	287	22	AAM55715
Human brain express	287	22	AAM55715
Human bone marrow	287	22	ABM15917
Peptide #2351 enco	287	22	ABM03653
Peptide #2315 enco	30	21	AAB18734
Transplant media a	30	23	AAU90987
Amino acid sequenc	36	21	AAB18727
Human novel secret	171	22	AAB16227
Human novel polype	171	24	ABU55341
GPR7 ligand relate	336	24	ABU37876
Neisseria meningit	723	21	AAY75477
Corynebacterium gil	288	22	ABP79222
C glutamamic prote	391	24	AAG92226
Arabidopsis thalia	590	23	AAB17085
Arabidopsis thalia	642	23	AAB17088
Transplant media a	29	23	AAU90944
Corynebacterium gil	269	22	ABT6593
C glutamamic prote	288	22	AAG90512
N. gonorrhoeae ami	403	9	ABP60274
Sequene of Creati	403	9	ABP80680
Creatine amidohyr	35.9	28	ABB83807
Large pulling toad			

## ALIGNMENTS

## RESULT 1

ID AAB18725 standard; Protein; 27 AA.  
 XX AAB18725; DT 22-JAN-2001 (first entry)  
 XX Amino acid sequence of mature\_protein\_dermaseptin b.  
 XX AC AAB18725;

XX Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;  
 KW cationic peptide; pathogen resistance.  
 XX Phyllomedusa bicolor.  
 XX PN WO200055337-A1.  
 XX PD 21-SEP-2000.  
 XX PF 16-MAR-2000; 2000WO-CA00288.  
 XX PR 17-MAR-1999; 99UG-0125072.  
 XX XX (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.  
 XX PA Misra S, Kay WD;  
 XX PI DR WPI; 2000-647077/62.  
 XX PT Transgenic plants resistant to broad spectrum of pathogens useful for  
 PT producing biologically active cationic peptides. Comprises nucleic acid  
 PT molecule encoding temporin and/or dermaseptin peptides -

XX Claim 3; Page 47; 58pp; English.

PS AAB18725-36 represent mature processed forms of dermaseptin. Dermaseptin

CC has antibacterial activity, and inhibits fungal growth. Cationic

CC peptides derived from temporins and dermaseptins are used to produce

CC transgenic plants. The transgenic plants are useful for producing

CC biologically active cationic peptides such as temporins and dermaseptins

CC in large quantities. The peptide confers broad spectrum pathogen

CC resistance including enhanced resistance to both fungal and bacterial

CC pathogens in the transgenic plants. The transgenic plants may be used

CC in conventional agricultural applications such as food crops, medical

CC and other applications.

XX Sequence 27 AA;

Query Match 100.0%; Score 128; DB 21; Length 31;

Best Local Similarity 100.0%; Pred. No. 1.3e-12;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVLKKGTVHALGKALGAVADTISQ 27

Db 5 DVLKKGTVHALGKALGAVADTISQ 31

RESULT 3

AAB12436

ID AAB12436 standard; peptide, 31 AA.

XX AAB12436

AC AAB12436;

XX 20-OCT-2000 (first entry)

XX Dermaseptin B amino acid sequence.

DB XX

KW CEMA; Pro-CEMA; dermaseptin B; temporin A; cecropin A; melittin;

KW CAMA 35S promoter; cationic polypeptide; antimicrobe; transgenic plant;

KW expression vector; agrobacillus; callus; phytopathogen; bacteria;

KW fungus; calli; antifungal; antibacterial.

XX Unidentified.

OS XX

XX CN1249310-A.

PN XX

XX 05-APR-2000.

PD XX

XX 28-SEP-1998; 98CN-0112269.

PR XX

XX 28-SEP-1998; 98CN-0112269.

PA (ZHOU/) ZHOU G.

XX

PI Zhou G;

XX

DR WPI; 2000-400710/35.

XX

PT Cationic polypeptide process for expressing antimicrobe in plant -

XX

PS Claim 2; Page 1; 7pp; Chinese.

XX

CC The present invention describes a transgenic plant expression vector

CC containing three antimicrobe cationic polypeptides. The plant tissue is

CC introduced to these genes via agrobacillus and in the callus culture,

CC the callus resisting phytopathogen (bacteria and fungus) can be

CC externally chosen. Choosing these calli can regenerate plants and

CC directly test its antifungal and antibacterial powder. After these

CC transgenic plants are ripened, whole or partial plant can be harvested.

CC The present sequence represents a specifically claimed peptide from

CC the present invention.

XX Sequence 31 AA;

Query Match 100.0%; Score 128; DB 21; Length 31;

Best Local Similarity 100.0%; Pred. No. 1.3e-12;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVLKKGTVHALGKALGAVADTISQ 27

Db 5 DVLKKGTVHALGKALGAVADTISQ 31

RESULT 4

AAB18748

ID AAB18748 standard; Protein; 32 AA.

XX AAB18748

AC AAB18748;

XX 22-JAN-2001 (first entry)

DS A mature dermaseptin protein with a N-terminal extension.  
 XX Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;  
 KW cationic peptide; pathogen resistance.  
 XX Synthetic.

OS *Phylomedusa bicolor*.  
 XX WO200055337-A1.

XX PD 21-SEP-2000.  
 XX PP 16-MAR-2000; 2000WO-CA00288.

XX PR 17-MAR-1999; 99US-0125072.  
 XX PA (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.

XX PI Misra S, Kay WD,  
 XX DR WPI; 2000-647077/62.

XX PN N-PSDB; AAA75749.  
 XX PR 16-MAR-2000; 2000WO-CA00288.

XX PR 17-MAR-1999; 99US-0125072.  
 XX PA (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.

XX PI Misra S, Kay WD,  
 XX DR WPI; 2000-647077/62.  
 XX N-PSDB; AAA75751.

XX PR 16-MAR-2000; 2000WO-CA00288.  
 XX PT Transgenic plants resistant to broad spectrum of pathogens useful for  
 PT producing biologically active cationic peptides. comprises nucleic acid  
 PT molecule encoding temporin and/or dermaseptin peptides

XX PS Example; Page 51; 58pp; English.

XX The present sequence represents a mature dermaseptin polypeptide  
 CC which has a N-terminal extension. Dermaseptin has antibacterial  
 CC activity, and inhibits fungal growth. Cationic peptides derived from  
 CC temporins and dermaseptins are used to produce transgenic plants. The  
 CC transgenic plants are useful for producing biologically active cationic  
 CC peptides such as temporins and dermaseptins in large quantities. The  
 CC peptide confers broad fungal and bacterial pathogens including enhanced  
 CC resistance to both fungal and bacterial pathogens in the transgenic  
 CC plants. The transgenic plants may be used in conventional agricultural  
 CC applications such as food crops, medical and other applications.

XX SQ Sequence 32 AA;

XX Query Match 100.0%; Score 128; DB 21; Length 32;  
 XX Best Local Similarity 100.0%; Pred. No. 1.3e-12;  
 XX Matches 27; Conservative 0; Mismatches 0;  
 XX Indels 0; Gaps 0;

XX Qy 1 DVLKIGTVLHAGKALGAVADTISQ 27  
 XX Db 6 DVLKIGTVLHAGKALGAVADTISQ 32.

XX RESULT 5

XX AAB18724 ID AAB18724 Standard; Protein; 78 AA.  
 XX AC AAB18724;  
 XX DT 22-JAN-2001 (first entry)

XX DE A dermaseptin precursor polypeptide.  
 XX KW Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;  
 KW cationic peptide; pathogen resistance.

XX OS *Phylomedusa bicolor*.  
 XX PN WO200055337-A1.

XX PD 21-SEP-2000.  
 XX PR 16-MAR-2000; 2000WO-CA00288.

XX PR 17-MAR-1999; 99US-0125072.

XX PN WO200055337-A1.

XX PD 21-SEP-2000.  
 XX PR 16-MAR-2000; 2000WO-CA00288.

XX PR 17-MAR-1999; 99US-0125072.

XX (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.  
 XX PA (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.  
 XX PI Misra S, Kay WD,  
 XX DR WPI; 2000-647077/62.  
 XX DR N-PSDB; AAA75749.  
 XX PR Transgenic plants resistant to broad spectrum of pathogens useful for  
 PR producing biologically active cationic peptides. comprises nucleic acid  
 PR molecule encoding temporin and/or dermaseptin peptides  
 XX Disclosure; Page 47; 58pp; English.  
 XX The present sequence represents a dermaseptin precursor polypeptide.  
 CC The precursor is processed to produce two mature forms, Dermaseptin b  
 CC (AAB18725) and dermaseptin B (AAB18726). Dermaseptin has antibacterial  
 CC activity, and inhibits fungal growth. Cationic peptides derived from  
 CC temporins and dermaseptins are used to produce transgenic plants. The  
 CC transgenic plants are useful for producing biologically active cationic  
 CC peptides such as temporins and dermaseptins in large quantities. The  
 CC peptide confers broad spectrum pathogen resistance including enhanced  
 CC resistance to both fungal and bacterial pathogens in the transgenic  
 CC plants. The transgenic plants may be used in conventional agricultural  
 CC applications such as food crops, medical and other applications.  
 XX SQ Sequence 78 AA;

XX Query Match 100.0%; Score 128; DB 21; Length 78;  
 XX Best Local Similarity 100.0%; Pred. No. 3.6e-12;  
 XX Matches 27; Conservative 0; Mismatches 0;  
 XX Indels 0; Gaps 0;  
 XX Qy 1 DVLKIGTVLHAGKALGAVADTISQ 27.  
 XX Db 49 DVLKIGTVLHAGKALGAVADTISQ 75  
 XX RESULT 6  
 XX AAY87380 ID AAY87380 Standard; peptide; 33 AA.  
 XX AC AAY87380;  
 XX DT 03-JUL-2000 (first entry)  
 XX DB Cationic antimicrobial peptide DER (frog dermaseptin), SEQ ID NO:23.  
 XX KW Antimicrobial; cationic; antibacterial; antiproliferative;  
 KW endotoxaemia; sepsis; wound repair; tissue regeneration;  
 KW transgenic animal; pathogen resistance.  
 XX OS Anura.  
 XX PN WO200012528-A1.  
 XX PD 09-MAR-2000.  
 XX PF 27-AUG-1999; 99WO-US19646.  
 XX PR 28-AUG-1998; 98US-0143124.  
 XX PA (UYBR-) UNIV BRITISH COLUMBIA.  
 XX PI Hancock REW, Gough MA, Patrykak A, Woods D, Jia X,  
 XX DR WPI; 2000-270790/23.  
 XX PT Novel anti-endotoxic, antimicrobial cationic peptides useful for  
 PT inhibiting endotoxin/sepsis associated disorder or cell  
 PT proliferation, accelerating wound healing, and treating respiratory  
 PT associated disorder  
 XX PS Claim 17; Page 93; 116pp; English.

XX The invention relates to a novel class of cationic antimicrobial nucleotides (AA87358-Y87391) and AA87383-Y87391). It also encompasses nucleotide sequences encoding the peptides and a transgenic animal comprising a nucleotide sequence encoding an anti-microbial peptide. The cationic antimicrobial peptides of the invention are useful for inhibiting the growth of Gram positive or Gram negative bacteria, in combination with an antibiotic or lysosome. The peptides are also useful for inhibiting the growth of a eukaryotic cell e.g., a neoplastic cell, and sequences AA87358-Y87369 may be used for inhibiting cell proliferation-associated disorders such as cancer. Peptides AA87358-Y87369 are useful for inhibiting endotoxaemia or a sepsis-associated disorder such as septic shock. The peptides of the invention may also be used for accelerating wound repair in a patient when coadministered with a healing agent such as TGF- $\beta$  (transforming growth factor-beta). The peptides are used for treating a respiratory or pulmonary-associated infection, or a disorder such as cystic fibrosis. The peptides are used for revitalising scar tissue, for wound repair in guided tissue degeneration (GTR) procedures, and for promoting tissue growth in skin grafts. Nucleic acids encoding peptides AA87372-Y87398 and AA87383-Y87391 may be used in the generation of transgenic animals, with nucleotide encoding sequences AA87372 and AA87374-Y87378 being particularly useful for the generation of transgenic fish with enhanced resistance to pathogenic organisms. Sequences AA87358-Y87381 and AA87383-Y87391 represent cationic antimicrobial peptides claimed for use in various embodiments of the invention.

XX Sequence 33 AA;

Query Match	85.9%	Score 110;	DB 21;	Length 33;
Best Local Similarity	84.6%;	Prod. No. 8e-10;		
Matches 22;	Conservative	3;	Mismatches 1;	Indels 0;
			Gaps 0;	

\*Qy 2 VLKKGITVALHAGKAALGAADTISQ 27  
DB :|||: :|||: |||: |||: |||:  
6 MLKKLGTMVALHAGKAALGAADTISQ 31

~ RESULT 7  
AAU90985 ID AAU90985 standard; Peptide; 33 AA.

AC AAU90985;

XX DT 05-JUN-2002 (first entry)

XX DB Transplant media associated antimicrobial peptide #21.  
XX KW Transplant; antimicrobial peptide; pore forming agent;  
KW cell surface receptor binding compound; kidney transplant;  
KW cardioplegia; organ transplant; transplant rejection.  
XX OS Phylomedusa sauvagei.  
XX PN WO200209738-A1.

XX PD 07-FEB-2002.

XX PP 27-JUL-2001; 2001WO-US23785.

XX PR 28-JUL-2000; 2000US-221632P.

PR 17-NOV-2000; 2000US-249603P.

PR 15-MAY-2001; 2001US-290913P.

XX PA (MURP) MURPHY C J.

XX PI Murphy CJ, Raid TW, Mcanulty JP,

DR WPI; 2002-268995/31.

XX Media comprising antimicrobial polypeptides or pore forming agents and/or cell surface receptor binding compounds useful for the storage and preservation of organs prior to transplant -

XX Disclosure; Page 26; 78pp; English.

XX The invention describes new transplant compositions comprising antimicrobial polypeptides or pore forming agents and/or cell surface receptor binding compounds. The media is capable of extending the preservation period past 72 hours and can provide organs with increased functionality upon transplant. Animals receiving kidneys stored in the media of the present invention for either three or four day had serum creatinine levels of less than half of those observed in control animals receiving kidneys stored in UW solution (defined in the specification) alone. Lower serum creatinine levels are indicative of healthier kidneys and more preferable prognosis for the transplant patient. The media of the invention are useful for decreasing the incidence and/or severity of delayed graft function in patients receiving transplanted kidneys stored and/or treated in the media. The media may also be used in procedures such as cardioplegia. It is contemplated that transplant of healthier organs leads to a decrease in chronic rejection. This sequence represents an antimicrobial peptide studied in the development of the transplant media.

XX Sequence 33 AA;

Query Match	85.9%	Score 110;	DB 23;	Length 33;
Best Local Similarity	84.6%;	Pred. No. 8e-10;		
Matches 22;	Conservative	3;	Mismatches 1;	Indels 0;
			Gaps 0;	

Qy 2 VLKKIGITVALHAGKAALGAADTISQ 27  
DB :|||: :|||: |||: |||: |||:  
6 MLKKLGTMVALHAGKAALGAADTISQ 31

RESULT 8  
AAB18732 ID AAB18732 standard; Protein; 34 AA.  
AC AAB18732;  
XX DT 22-JAN-2001 (first entry)  
XX DE Amino acid sequence of a mature processed form of dermaseptin.  
XX KW Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant; cationic Peptide; pathogen resistance.  
XX OS Phylomedusa sauvagei.  
XX PN WO200055337-A1.  
XX PR 21-SEP-2000.  
XX PD 16-MAR-2000; 2000WO-CA00288.  
XX PR 17-MAR-1999; 99US-0125072.  
XX PA (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.  
XX PI Misra S, Kay WD;  
XX DR WPI; 2000-647077/62.  
XX PT Transgenic plants resistant to broad spectrum of pathogens useful for producing biologically active cationic peptides, comprises nucleic acid molecule encoding temporin and/or dermaseptin peptides -  
XX PS Claim 3; Page 49; 58pp; English.  
XX AAB18725-36 represent mature processed forms of dermaseptin. Dermaseptin has antibacterial activity, and inhibits fungal growth. Cationic peptides derived from temporin and dermaseptins are used to produce transgenic plants. The transgenic plants are useful for producing biologically active cationic Peptides such as temporins and dermaseptins in large quantities. The peptide confers broad spectrum pathogen

CC resistance including enhanced resistance to both fungal and bacterial  
 CC pathogens in the transgenic plants. The transgenic plants may be used  
 CC in conventional agricultural applications such as food crops, medical  
 XX and other applications.

XX SQ sequence 34 AA;

Query Match 2 VLIKIGITVALHAGKAALGAVADTISQ 27  
 Best Local Similarity 85.9%; Score 110; DB 22; Length 34;  
 Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VLIKIGITVALHAGKAALGAVADTISQ 27  
 Db :|||:|||||:|||||:|||||:|||||:  
 6 MLKKLGTMALHAGKAALGAVADTISQ 31

RESULT 9  
 AAB91864 DT 14-MAY-2003 (first entry)  
 ID AAB91864 Standard; Peptide; 34 AA.  
 XX AC AAB91864;  
 XX DT 22-JUN-2001 (first entry)  
 DE Antimicrobial peptide SEQ ID NO:1040.  
 XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimidyl; maleimido group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
 XX OS Homo sapiens.  
 OS Synthetic.  
 PN WO200069900-A2.  
 XX PD 23-NOV-2000.  
 PD 17-MAY-2000; 2000WO-US13576.  
 XX PR 17-MAY-1999; 99US-0134406.  
 PR 10-SEP-1999; 99US-0153406.  
 PR 15-OCT-1999; 99US-0159783.  
 PA (CONJ-) CONJUCHEM INC.  
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;  
 XX PS Example 5; Fig 5; 50pp; English.  
 DR WPI; 2001-112059/12.

XX PT Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity  
 PT  
 XX Disclosure; Page 535; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutic peptide (II) (e.g. succinimidyl and maleimido groups) attached to  
 CC a reactive group (III) (e.g. succinimidyl and maleimido groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxy/thiol groups on blood components to form a  
 CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity  
 CC in vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidase to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention.

SQ Sequence 34 AA;  
 Query Match 2 VLIKIGITVALHAGKAALGAVADTISQ 27  
 Best Local Similarity 85.9%; Score 110; DB 22; Length 34;  
 Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VLIKIGITVALHAGKAALGAVADTISQ 27  
 Db :|||:|||||:|||||:|||||:  
 6 MLKKLGTMALHAGKAALGAVADTISQ 31

RESULT 10  
 AAE34434 DT 14-MAY-2003 (first entry)  
 ID AAE34434 Standard; peptide; 34 AA.  
 XX AC AAE34434;  
 XX PR dermaseptin peptide.  
 KW Antimicrobial; purple blotch; gene therapy; antibacterial; fungicide;  
 KW frog; dermaseptin.  
 XX OS Rana sp.  
 PN WO200295076-A2.  
 XX PD 28-NOV-2002.  
 PF 17-MAY-2002; 2002WO-JP04800.  
 PR 23-MAY-2001; 2001JP-0154321.  
 PR 26-DEC-2001; 2001JP-0394821.  
 PA (TOKY ) TOYOTA CHUO KENKYUSHO KK.  
 XX PI Muranoto N, Imaeda T, Hirai M, Shimamura T;  
 DR WPI; 2003-156762/15.  
 XX New polypeptide comprising at least one protease-resistant or  
 PT protease-sensitive sequence, bound to the C-terminal side of the target  
 PT polypeptide, useful as antimicrobial agent against Ceratocystis  
 PT fimbriata, or Escherichia coli. They are also used in gene therapy.  
 CC The present sequence is frog dermaseptin peptide used in the  
 CC exemplification of the invention.  
 XX PS Example 14; Fig 5; 50pp; English.  
 XX

The invention relates to a polypeptide comprising at least one protease-  
 CC resistant or protease-sensitive sequence, bound to the C-terminal side  
 CC of the target polypeptide. The polypeptides are useful as antimicrobial  
 CC agents against Ceratocystis fimbriata which causes purple blotch in  
 CC sweet potatoes, or Escherichia coli. They are also used in gene therapy.  
 CC The present sequence is frog dermaseptin peptide used in the  
 CC exemplification of the invention.

XX SQ Sequence 34 AA;

Query Match 2 VLIKIGITVALHAGKAALGAVADTISQ 27  
 Best Local Similarity 85.9%; Score 110; DB 24; Length 34;  
 Matches 22; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VLIKIGITVALHAGKAALGAVADTISQ 27  
 Db :|||:|||||:|||||:  
 6 MLKKLGTMALHAGKAALGAVADTISQ 31

RESULT 11  
 AAB18733 ID AAB18733 Standard; Protein; 34 AA.  
 XX AC AAB18733;  
 XX

DT 22-JAN-2001 (first entry)  
 XX Amino acid sequence of a mature processed form of dermaseptin.  
 DE XX  
 PR 28-JUL-2000; 2000US-221632P.  
 PR 17-NOV-2000; 2000US-249603P.  
 PR 15-MAY-2001; 2001US-290932P.  
 KW Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;  
 KW cationic peptide; pathogen resistance.  
 XX Phylomedusa sauvagei.  
 OS XX  
 PR Murphy CJ, Reid TW, Mcanulty JF;  
 XX  
 PN WO200055337-A1.  
 XX  
 PA (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.  
 XX  
 PI Misra S, Kay WD;  
 XX DR WPI, 2000-647077/62.  
 XX PT Transgenic plants resistant to broad spectrum of pathogens useful for  
 PT producing biologically active cationic peptides, comprises nucleic acid  
 PT molecule encoding temporin and/or dermaseptin peptides -  
 XX PS Claim 3; Page 49; 589P; English.  
 XX AAB18725-36 represent mature processed forms of dermaseptin. Dermaseptin  
 CC has antibacterial activity, and inhibits fungal growth. Cationic  
 CC peptides derived from temporins and dermaseptins are used to produce  
 CC transgenic plants. The transgenic plants are useful for producing  
 CC biologically active cationic peptides such as temporins and dermaseptins  
 CC in large quantities. The peptide confers broad spectrum pathogen  
 CC resistance including enhanced resistance to both fungal and bacterial  
 CC pathogens in the transgenic plants. The transgenic plants may be used  
 CC in conventional agricultural applications such as food crops, medical  
 CC and other applications.  
 XX SQ Sequence 34 AA;  
 Query Match 82.0%; Score 105; DB 21; Length 34;  
 Best Local Similarity 80.8%; Pred. No. 4.9e-09;  
 Matches 21; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 YY 2 VLKKGTVVALHAGKALGAVADTISQ 27  
 :|||:|||:|||:|||:|||:|||:  
 Db 6 MLKKLGTMHALHAGKALGAVADTISQ 31  
 AC AAW66438;  
 XX RESULT 13  
 AAW66438 DT 12-JAN-1999 (first entry)  
 XX ID AAW66438 standard; peptide; 32 AA.  
 XX DB AAW66438 standard; peptide; 32 AA.  
 XX AC AAW66438;  
 XX KW Indolicidin analogue; resistance; cationic peptide; antibiotic;  
 KW bacteria; fungicide; tolerance; antibiotic; microorganism;  
 KW parasite; virus.  
 XX OS Phylomedusa sauvagei.  
 XX PN WO9840401-A2.  
 XX PD 17-SEP-1998.  
 PR 25-FEB-1998; 98W0-CA00190.  
 PR 10-MAR-1998; 98W0-CA00190.  
 PR 10-MAR-1998; 98W0-CA00190.  
 PR 10-MAR-1997; 97W0-0040649.  
 PR 20-AUG-1997; 97W0-0915314.  
 PR 26-SEP-1997; 97W0-0660099.  
 PA (MICR-) MICROLOGIX BIOTECH INC.

Invention relates to a pharmaceutical composition containing at least one activated polyoxyalkylene (APO)-modified cationic peptide. The modification of peptides with APO increases their activity against tumour cells, including those with a multidrug resistant phenotype. The pharmaceutical composition can be used to treat tumours, specifically lymphoma, leukaemia, multiple myeloma, or tumours of breast, lung, ovary, cervix, uterus, skin, prostate, liver and colon.

CC AAW66193 to AAW66169 represent native cationic peptides from the  
 CC present invention. The present invention describes compositions and  
 CC methods for treating infection, especially bacterial infections. The  
 CC compositions and methods use cationic peptides in combination with an  
 CC antibiotic agent which are then administered to a patient to enhance the  
 CC activity of the antibiotic agent to overcome: (a) tolerance; (b)  
 CC acquired resistance; and (c) inherent resistance. The combinations of  
 CC antibiotics and cationic peptides can provide synergistic activity  
 CC against a microorganism that is tolerant, inherently resistant, or has  
 CC acquired resistance to an antibiotic agent. They can be used for killing  
 e.g. bacteria, fungi, parasites and viruses.

Query Match      / / : \* ;    Score 99.5 ;    DB 21 ;    Length 32 ;  
 Best Local Similarity 84.6% ;    Pred. No. 3.2e-08 ;  
 Matches 22 ;    Conservative 3 ;    Mismatches 0 ;    Gaps 1 ;  
 Indels 1 ;

1 U59614 standard; Peptide, 32 AA.  
 2 VLRKIGTVLHAGKALGAVADTISQ 27  
 :|:||:|||||:|||:|||:|||:  
 6 MLRKIGTVLHAGKALGAVADTISQ 30

RESULT 14  
 AAY91737  
 ID AAY91737 standard; Peptide; 32 AA.  
 XX  
 XX  
 AC AC  
 HX HX  
 DDT DDT  
 XX  
 XX  
 DE DE  
 KK KK  
 KW KW  
 KW KW  
 KW KW  
 KW KW  
 KW KW  
 Cationic Peptide; tumour; pharmaceutical composition; cancer; treatment  
 leukaemia; polyoxazoline-modified; APO; lymphoma; multiple myeloma;  
 breast; lung; ovary; cervix; uterus; skin; prostate; liver; colon;  
 multidrug resistance.

Synthetic.			
US2002041898-A1.			
11-APR-2002.			
25-JUL-2001; 2001US-0912609.			
05-JAN-2000; 2000US-0478124.			
31-OCT-2000; 2000US-0703474.			
(UNGE /) UNGER E C.	Ramaseswami V,	Ramaseswami V,	Romanowski MJ;
(MATS /) MATSUNAGA T O.			
(RAMA /) RAMASWAMI V.			
(ROMA /) ROMANOWSKI M J.			
Unger EC,	Matsunaga TO,		

Novel pharmaceutical composition containing optionally activated polyoxalkylene-modified cationic peptides, useful for treating tumours

INN:	Ketotifen fumarate		
AN:	KXX		
BN:	KXX		
CPD:	23-DEC-1999.		
CPX:			
CPF:	14-JUN-1999;	99WO-CA00552.	
CPI:			
PRR:	12-JUN-1998;	98US-0096541.	
PRX:			
PRY:			
(MICR-)	MICROLOGIX BIOTECH INC.		
PRI:	Friedland HD,	Krieger TJ,	Taylor R,
PRF:	Erfle D,	Fraser JR,	West MHP,
WPI:	2000-223549/19.		

WPI; 2003-208921/20.  
Targeted delivery system comprising a bioactive agent homogeneously dispersed in a targeted matrix is especially useful in cancer therapy

Disclosure: Page14; 46pp; English.

The invention relates to a composition comprising a bioactive agent homogeneously dispersed in a targeted matrix (polymer and targeting ligand). Also included are a targeted matrix for use as a delivery vehicle comprising a polymer associated with a targeting ligand, enhancing the bioavailability of an agent comprising administration of the composition and treating cancer comprising administration of the novel composition. The method is useful for targeted delivery of a drug, especially in cancer therapy. The targeting ligand may be a peptide. Examples of targeting peptides are disclosed including cathepsin-D substrate peptides, peptides targeting receptors in the brain and kidney, peptides recognising fibronectin- and vitronactin-binding integrins, peptides targeting the RGD (Arg-Gly-Asp) motif in, e.g., antibodies, peptides targeting the Arg-Gly-Asp motif in fibronectin, laminin, heparan sulphate proteoglycans, etc.

Pr  
Ct  
PS  
PS  
CC  
CC  
This sequence represents a cationic peptide amino acid sequence, which can be used in the pharmaceutical composition of the invention. The disclosure; Page 11; 94pp; English.

CC tumours, tissue specific peptides (e.g. of lung, skin, pancreas,  
CC intestine, uterus, adrenal gland and retina), and cationic cancer-  
CC targeting peptides. The present sequence is a peptide targeting  
CC ligand disclosed in the invention.

XX Sequence 32 AA;

Query Match 77.7%; Score 99.5; DB 24; Length 32;  
Best Local Similarity 84.6%; Pred. No. 3.2e-08;  
Matches 22; Conservative 3; Mismatches 0; Indels 1; Gaps 1;  
Qy 2 VLXKIGTVALHAGKAALGAVADISQ 27  
:|||||:|||||:|||||:|||||:  
Db 6 MLXKIGTVALHAGKAALGAVADISQ 30

Search completed: December 10, 2003, 20:27:42  
Job time : 42 secs